

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 5, 2004, 02:13:54 ; Search time 1520.27 Seconds
(without alignments)
3592.268 Million cell updates/sec

Title: US-10-005-429-14

Perfect score: 652

Sequence: 1 MAABEGAVIACHTKDFDAR.....DAVRKYAAAGTTTAPASASA 126

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO.spool.p/US10005429/runat_04052004_121649_15437/app.query.fasta_1.782
-DB=GenEmbl -QFWT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40 cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10005429.cgn2_1_15417 @runat_04052004_121649_15437 -NCPU=6 -ICPU=3
-NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl:

1: gb.ba:*
2: gb.htg:*
3: gb.in:*
4: gb.om:*
5: gb.ov:*
6: gb.pat:*
7: gb.ph:*
8: gb.pl:*
9: gb.pr:*
10: gb.ro:*
11: gb.sts:*
12: gb.sy:*
13: gb.un:*
14: gb.vi:*
15: em.ba:*
16: em.fun:*
17: em.hum:*
18: em.in:*
19: em.mu:*
20: em.om:*
21: em.or:*
22: em.ov:*
23: em.pat:*
24: em.ph:*
25: em.pl:*
26: em.ro:*
27: em.scs:*
28: em.un:*

RESULT 1

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	361	55.4	526	11	G73679 RZ498R etio
2	361	55.4	600	8	AK059196 Oryza sat
3	361	55.4	601	8	U92541 Oryza sativ
4	361	55.4	686	6	E08194 RPS13 Gene
5	361	55.4	687	8	D21836 Oryza sativ
6	361	55.4	733	8	AK121423 Oryza sat
7	338	51.8	357	8	AY245454 Hordeum v
8	333	51.1	598	8	AY072771 Triticum
9	315	48.3	466	6	AB414207 Sequence
10	315	48.3	466	6	BD109760 EST and e
11	306.5	47.0	590	6	AY088698 Arabidops
12	305.5	46.9	360	6	AX505469 Sequence
13	305.5	46.9	360	8	BT004710 Arabidops
14	305.5	46.9	556	8	AK118542 Arabidops
15	301.5	46.2	642	8	Z35473 A.thaliana
16	285	43.7	564	8	AF333593 Prunus pe
17	284	43.6	345	8	AF433265 Populus t
18	282	43.3	345	6	AX505468 Sequence
19	282	43.3	480	8	AY088687 Arabidops
20	282	43.3	497	8	Z14084 A.thaliana
21	278	42.6	676	8	AY344230 Ipomoea b
22	275.5	42.3	580	8	BNU59380 Brassica na
23	272	41.7	731	8	AY344229 Ipomoea b
24	272	41.7	784	8	AY344229 Citrus x
25	271	41.6	698	8	NTTRNA
26	267	41.0	603	8	RCTHIOXN
27	262	40.2	596	8	TAE9762 Triticum
28	261	40.0	653	6	AR016869 Sequence
29	261	40.0	653	6	AR020895 Sequence
30	261	40.0	653	6	AR027218 Sequence
31	261	40.0	653	6	AR036505 Sequence
32	261	40.0	653	6	AR064647 Sequence
33	261	40.0	653	6	AR067572 Sequence
34	261	40.0	653	6	I38524 Sequence 10
35	261	40.0	653	6	I56999 Sequence 10
36	261	40.0	653	6	I59865 Sequence 10
37	261	40.0	653	6	I75192 Sequence 10
38	261	40.0	653	6	AR403740 Sequence
39	259.5	39.8	595	8	D87984 Paspalum e
40	256.5	39.3	641	8	AF051206 Picea mar
41	254	39.0	366	8	AX654096 Sequence
42	254	39.0	682	8	AK059385 Oryza sat
43	254	39.0	740	8	AB053294 Oryza sat
44	254	39.0	3740	8	AK106758 Oryza sat
45	253	38.8	357	8	AY040028 Arabidops

ALIGNMENTS

G73679 526 bp DNA linear STS 16-JUL-2002
 RZ488R etiolated leaf tissue of rice *Oryza sativa* STS genomic clone
 RZ488 sequencing direction=reverse, sequence tagged site.
 G73679
 G73679.1 GI:19697274
 STS.
Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae;
Ehrhartoideae; *Oryzaceae*; *Oryza*.
 1 (bases 1 to 526)
 McCouch, S.R.
Oryza sativa STS
 Unpublished (2002)
 JOURNAL
 COMMENT
 Contact: Susan R. McCouch
 Cornell University
 Dept. of Plant Breeding, Ithaca, NY 14853-1901, USA
 Tel.: 6072550420
 Fax: 6072556683
 Email: srm4@cornell.edu
 Primer A: M13 universal Forward GTAAACGACGGCCAGT
 Primer B: M13 universal Reverse AACAGTATGACCATG
 STS size: 526
 Protocol:
 Template: 20-100ng
 Primer: 5pmol each
 DMTs: 40nmol
 Taq polymerase: 5units
 Total volume: 50ul
 Buffer:
 Tris-HCl: 100mM
 KCl: 500mM
 MgCl2: 15mM
 Gelatin: 0.1%
 PH: 8.3
 This is a partial sequence of the RFLP clone named above that was
 mapped at Cornell University Plant Breeding Dept. and sequenced at
 the Genome Sequencing Center at Cold Spring Harbor Laboratory. This
 marker is located on rice chromosome 7. For citations and other
 related information concerning this probe, please refer to the
 Gramene database at <http://www.gramene.org>
 Location/Qualifiers
 1..526
 /organism="Oryza sativa (indica cultivar-group)"
 /mol_type="genomic DNA"
 /cultivar="IR36"
 /db_xref="taxon:39946"
 /map="7"
 /clones="RZ488"
 /clone_lib="etiolated leaf tissue of rice"
 /note="Vector: Lambda ZAP II/pBluescript; V-type: Plasmid;
 A Lambda ZAP II cDNA library was constructed from mRNA
 extracted from etiolated leaf tissue of the rice cultivar
 IR36 and converted to pBluescript (amp resistant) as
 described in Cause et al. (1994) Genetics 138:1251-1274.
 For insert amplification, Use M13 forward and reverse
 primers. Restriction site is EcoRI. Clones from this
 library are designated with the prefix 'RZ'."
 <1..>526
 STS
 ORIGIN
 Alignment Scores:
 Pred. No.: 7,55e-34 Length: 526
 Score: 361.00 Matches: 70
 Percent Similarity: 71.77% Conservative: 19
 Best Local Similarity: 56.45% Mismatches: 33
 Query Match: 55.37% Indels: 2
 DB: 11 Gaps: 1

US-10-005-429-14 (1-126) x G73679 (1-526)
 QY 1 MetAlaAlaGluGluGlyAlaValValleAlaCyShisThrLyAspGluPheAspAlaArg 20
 DB 83 ATGGCCGCGGAGGGAGTGTGATCCCTGCCCAACAGGACGAGTTCACCCGAG 142
 QY 21 MetAlaAlaLysGluGluGlyLysLeuValValleAlaAspPheMetAlaProTrpCys 40
 DB 143 ATGACCAAGGCCAGGAGCGCGCAAGTGTGATATTTGACTTCCTTCCTGCTGT 202
 QY 41 SerGlyCysGlnMetMetAlaProValTyrAlaAspCysAlaSerLysTyrProSerAla 60
 DB 203 GGCCTTCGCGCTTCATCGCCCGAGTGTGCTGAATACGCCAAAGTTCCTCGTGT 262
 QY 61 ValPheLeuGluValAspValAspGluLeuValAlaLysLeuValLysLeuValHis 80
 DB 263 GTCTTCTGAGGTTGATGTTGATGCTGAAGGAGTGTGCTGAAGGATCAATGTTGAG 322
 QY 81 ValMetProThrPheCysPheIleArgSenglyGluThrLeuGluSerPheAlaThrVal 100
 DB 323 GCAATGCCGACCTTCTTATTCATCAAGGATGTGCTGAGGCTGCAAGGCTGTGGCGCC 382
 QY 101 AspGluAspGluLeuArgAspAlaValArgLysTyrAlaAlaAlaGlyThrThrAla 120
 DB 383 AGAAGGATGACCTTCAGAACACCATGTGAAGCAC-----GTGGTGCCTGCTGCA 436
 QY 121 ProAlaSerAla 124
 DB 437 TCTGTTCTGCCC 448
 RESULT 2
 AK059196
 LOCUS
 DEFINITION
 Oryza sativa (japonica cultivar-group) cDNA clone:001-024-A03, full
 insert sequence.
 AK059196
 AK059196.1 GI:32969214
 VERSION
 FLI CDNA: oligo-capping.
 KEYWORDS
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae;
Ehrhartoideae; *Oryzaceae*; *Oryza*.
 REFERENCE
 1
 The Rice Full-length cDNA Consortium, National Institute of
 Agrobiological Sciences Rice Full-length cDNA Project Team;
 Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K.,
 Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I.,
 Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C.,
 Ohtsuki, K., Shishiki, T., Foundation of Advancement of International
 Science Genome Sequencing & Analysis Group; Ohtsuki, K., Murakami, K.,
 Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y.,
 Kuraaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M.,
 Narikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Niikura, J.,
 Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Miura, J.,
 Kusumegi, T., Okami, P., Ryu, R., Ueda, M., Matsubara, K., RIKEN;
 Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S.,
 Kura, A., Hashidume, W., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M.,
 Kaga, I., Kondo, S., Konno, H., Miyazaki, A., Osato, N., Ota, Y.,
 Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T.,
 Yoshino, M., and Hayashizaki, Y.
 Collection, mapping, and annotation of over 28,000 cDNA clones from
 Japonica rice
 Science 301 (5631), 376-379 (2003)
 JOURNAL
 MEDLINE
 PUBMED
 12869764
 REFERENCE
 2 (bases 1 to 600)
 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K.,
 Fujimura, T., Fukuda, S., Hanganaki, T., Hara, A., Hashizume, M.,
 Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hiraoka, T.,
 Hori, F., Hotta, I., Iida, J., Ikeda, R., Imamura, K.,
 Imotani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I.,

QY	1	MetAlaAlaGluGluGlyValAlaValileAlaCysHisThrLyAspGluPheAspAlaArg	20
Db	86	ATGCGCGCGAGGAGTGGTATCGCTTCGTCACCAACAGGACGAGTTCGACGCCAG	145
QY	21	MetAlaLyAsAlaLySGluGluGlyLysLeuValValileAspPheMetAlaProTTPCys	40
Db	146	ATGACACAGGCCAGAGAGCGCCGCAAGGTGTCAATATGACTTCACTGCTTCTGGTGT	205
QY	41	SerGlyCysGlnMetMetAlaProValTyrAlaAspCysAlaSerLysTyrProSerAla	160
Db	206	GGCCCTTCGCGCTTCATCGCCCACTGTCGTATGATACGCCAAAAGATTCCCTGGTGT	265
QY	61	ValPheLeuGluValAspValAspGluLeuLeuGluValAlaLysIleTyrGlyValHis	80
Db	266	GTCCTTCCTGAAGGTGTGTGATGAGCTGAAGGAGTGTCTGAAAGTACAATGTCGAG	325
QY	81	ValMetProThrPheCysPheIleArgAsnGlyGluThrLeuGluSerPheAlaThrVal	100
Db	326	GCAATGCCGACCTTCCTATTTCATCAAGGATGCTGAGGCTGCACAGGTCGTTGGCGC	385
QY	101	AspGluAspGluLeuArgAspAlaValArgLysTyrAlaAlaAlaGlyThrThrAla	120
Db	386	AGGAGGATGACCTTCAGAACACCATCTGAAGCAC-----GTCGGTGCCACTGCTGCA	439
QY	121	ProAlaSerAla 124	
Db	440	TCTGCTTCTGCC 451	
RESULT 4			
LOCUS	E08194		
DEFINITION	RPS13 gene encoding sieve tube protein.	686 bp	RNA
ACCESSION	E08194		linear
VERSION	E08194.1	GI:2176315	
KEYWORDS	JP 1994269286-A/1.		
SOURCE	unidentified		
ORGANISM	unclassified.		
REFERENCE	1 (bases 1 to 686)		
AUTHORS	Kayano,M.		
TITLE	SIEVE TUBE PROTEIN GENE OF PLANT AND METHOD FOR MAKING USEFUL		
JOURNAL	PROTEIN TRANSMIGRATE TO SIEVE TUBE USING THE SAME		
COMMENT	Patent: JP 1994269286-A 1 27-SEP-1994; MITSUI GIYOUSAI SHOKUBUTSU BIO KENKYUSHO:KK OS Oryza sativa L., var. aichiasahi PN JP 1994269286-A/1 PD 27-SEP-1994 PF 19-MAR-1993 JP 1993060763 PI KAYANO MITSUO PC C12N15/29,A01H5/00,C12P21/02//C12N5/10; CC strandedness: Double; CC topology: Linear; CC Feature is identified by other; FH Key Location/Qualifiers FT source FT 1. .686 FT /organism='Oryza sativa L., var. aichiasahi', FT /tissue_type='leaf', FT /clone='CRSP13-1', FT 5'UTR FT 1. .56 FT COS FT 57. .425 FT /product='sieve tube protein' FT 3'UTR FT 426. .686. FT Location/Qualifiers FT 1. .686 FT /organism='unidentified' FT /mol_type='genomic RNA' FT /db_xref='taxon:32644'		
FEATURES			
source			
ORIGIN			
Alignment Scores:			


```

source      1. .733
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="J023133N23"

ORIGIN
Alignment Scores:
Pred. No.:      1,11e-33      Length:      733
Score:          361.00      Matches:      70
Percent Similarity: 71.77%      Conservative: 19
Best Local Similarity: 56.45%      Mismatches:  33
Query Match:    55.37%      Indels:      2
DB:              8      Gaps:         1

US-10-005-429-14 (1-126) x AK121423 (1-733)
Qy      1 MetAlaLaGluGluGluValAlaValAlaCysHisThrLysAspGluPheAspAlaArg 20
Db      95 ATGCCCCCGAGGAGGAGTGGTATCCCTGCCACACAGGACGAGTTTCGAGGCCAG 154
Qy      21 MetAlaLysAlaLysGluGluGluValValAlaLysPheMetAlaProTyrCys 40
Db      155 ATGACCAAGGCCAAGGAGGCGGCAAGTGGTCATAATTGACTTCACCTGCTTCCTGCTGT 214
Qy      41 SerGlyCysGlnMetMetAlaProValTyrAlaAspCysAlaSerLysTyrProSerAla 60
Db      215 GGCCCTTTCGCCGCTTCATCGCCCCAGTGTTCCTGAATACGCCAAAAGTTCCCTCGTGTCT 274
Qy      61 ValPheLeuGluValAspValAspGluLeuLeuGluValAlaLysIleTyrGlyValHis 80
Db      275 GTCTTCCTGAGGTTGATGTTGATGAGCTGAAGGAGTTGCTGAAAGATCAATGTCTGAG 334
Qy      81 ValMetProThrPheCysPheIleArgAsnGlyGluThrLeuGluSerPheAlaThrVal 100
Db      335 GCAATGCGCGACTTCCTATTCAATCAAGGATGCTGAGCTGCAAGAGTCTGTGGCGCC 394
Qy      101 AspGluAspGluLeuArgAspAlaValArgLysTyrAlaAlaLysIleTyrThrAla 120
Db      395 AGGAGATGATGACCTCCAGAACACCATCTGTGAGGAC-----GTGCGTGCCACTGTGCA 448
Qy      121 ProAlaSerAla 124
Db      449 TCTGCTTCTGCC 460

RESULT 7
AY245454
LOCUS      Hordeum vulgare subsp. vulgare thioresdoxin h isoform 1 mRNA,
DEFINITION complete cds.
ACCESSION AY245454.1 GI:32186039
VERSION
KEYWORDS
SOURCE
ORGANISM
Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.
1 (bases 1 to 357)
REFERENCE
AUTHORS      Maeda K., Finnie C., Ostergaard O. and Svensson B.
TITLE      Identification, cloning and characterization of two thioresdoxin h
JOURNAL      isoforms, HvTrxh1 and HvTrxh2, from the barley seed proteome
MEDLINE      Eur. J. Biochem. 270 (12), 2633-2643 (2003)
PUBMED      22671460
12787030
REFERENCE
AUTHORS      Maeda K., Finnie C., Ostergaard O. and Svensson B.
TITLE      Direct Submission
JOURNAL      Submitted (21-FEB-2003) Chemistry, Carlsberg Laboratory, Gamle
Carlsberg Vej 10, Copenhagen DK-2500 Valby, Denmark
FEATURES
location/Qualifiers
1..357
source

/organism="Hordeum vulgare subsp. vulgare"
/mol_type="mRNA"
/cultivar="barke"
/sub_species="vulgare"
/db_xref="taxon:112509"
/dev_stage="embryo"
1..357
/notes="protein disulfide reductase; HvTrxh1"
/codon_start=1
/product="thioresdoxin h isoform 1"
/protein_id="AAP72290.1"
/db_xref="GI:32186040"
/translation="MAAEAGAVIACHTKQEPDTHMANGXDTKLVIIIDFTASWCGPCR
VIAPVFAEVAKFPAGAIPLUKVDVDELKDVAEAYNVEMPTFLFKDGEKVDVSVGGGRK
DDIHTKIVALNGSAST"

ORIGIN
Alignment Scores:
Pred. No.:      2,71e-31      Length:      357
Score:          338.00      Matches:      62
Percent Similarity: 71.19%      Conservative: 22
Best Local Similarity: 52.54%      Mismatches:  34
Query Match:    51.84%      Indels:      0
DB:              8      Gaps:         0

US-10-005-429-14 (1-126) x AY245454 (1-357)
Qy      1 MetAlaLaGluGluGluValAlaValAlaCysHisThrLysAspGluPheAspAlaArg 20
Db      1 ATGCCCCCGAGGAGGAGGCGTTCATCGCTGCCACACAGGACGAGTTTCGATACCCAC 60
Qy      21 MetAlaLysAlaLysGluGluGluValValAlaLysPheMetAlaProTyrCys 40
Db      61 ATGCGCAATGCGCAAGGACACCGGCAAGTGGTGTATCATTTCACTTCTCTCTGCTGC 120
Qy      41 SerGlyCysGlnMetMetAlaProValTyrAlaAspCysAlaSerLysTyrProSerAla 60
Db      121 GTGCCATGCTGTCTATGATGAGCTGAGTGTTCGTCGAGTACGAGGAGTTCCTCGGCGCC 180
Qy      61 ValPheLeuGluValAspValAspGluLeuLeuGluValAlaLysIleTyrGlyValHis 80
Db      181 ATCTTCTGAGGTGGATGTTGATGAGCTGAGGAGCTGCTGAGGACATACATATGTGAG 240
Qy      81 ValMetProThrPheCysPheIleArgAsnGlyGluThrLeuGluSerPheAlaThrVal 100
Db      241 GCAATGCGCGACTTCCTGTTTATCAAGGACGCTGAGGAGTGTGTCGCTGCTGCTGCTG 300
Qy      101 AspGluAspGluLeuArgAspAlaValArgLysTyrAlaAlaLysIleTyrThr 118
Db      301 AGGAGATGATGACATCCATCCAGATGAGTGGCCCTCATGGGTTCTGCATCCACC 354

RESULT 8
AY072771
LOCUS      Triticum aestivum cultivar Soissons thioresdoxin H mRNA, complete
DEFINITION cds.
ACCESSION AY072771
VERSION
KEYWORDS
SOURCE
ORGANISM
Triticum aestivum (bread wheat)
Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
1 (bases 1 to 598)
REFERENCE
AUTHORS      Cazalis R.
TITLE      Triticum aestivum thioresdoxin H
JOURNAL      Unpublished
REFERENCE
AUTHORS      Cazalis R.
TITLE      Direct Submission
JOURNAL      Submitted (10-JAN-2002) Plant Physiology, ESA Purpan, 75 voie du
TOEC, Toulouse 31076, France

```

FEATURES

source
Location/Qualifiers
1. .598
/organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="Soissons"
/db_xref="taxon:4565"
/dev_stage="28 day after anthesis developing seed"
1. .357
/note="redox protein; Trxh; similar to Oryza sativa thioredoxin H"
/codon_start=1
/product="thioredoxin H"
/protein_id="AA167139.1"
/db_xref="GI:27461140"
/translation="MAAEEGAVIACHTKQSEFTHWANGKETGKLVIIPTASWCQPCR
VIAPFAVYAKFPFGAIFLKVDVDELDVAEAYNVEAMPTFLFKDKAKVDVTWVGK
DDIHTKIVALMGSA"

ORIGIN

Alignment Scores:
Pred. No.: 1.95e-30 Length: 598
Score: 333.00 Matches: 63
Percent Similarity: 70.83% Conservative: 22
Best Local Similarity: 52.50% Mismatches: 33
Query Match: 51.07% Indels: 2
DB: 8 Gaps: 1

US-10-005-429-14 (1-126) x AY072771 (1-598)

QY 1 MetAlaAGluGluGluValAlaValIleAlaCysHisThrLysAspGluPheAspAlaArg 20
DB 1 ATGGCGCGCAGGAGGAGCGGTGATAGTGGCCACACCAAGAGTTCGACCCAC 60
QY 21 MetAlaLysAlaLysGluGlnGlyLysLeuValValIleAspPheMetAlaProThrCys 40
DB 61 ATGGCTAATGCGAAGGAGACCGCAAGCTGGTATCATTGACTTCACTCTTCCTGGTGC 120
QY 41 SerGlyCysGlnMetMetAlaProValTyrAlaAspCysAlaSerLysTyrProSerAla 60
DB 121 GGTCTTGTGCTATAGCCCGAGTCTTGTGATAGCCCAAGAGTTCCTGGCGC 180
QY 61 ValPheLeuGluValAspValAspGluLeuLeuGluValAlaLysIleTyrGlyValHis 80
DB 181 ATTTCCTGAAGTGGACGCTGACGAGCTGAAGGACGCTGACGATACACCAAGCTTGAG 240
QY 81 ValMetProThrPheCysPheIleArgAsnGlyGluThrLeuGluSerPheAlaThrVal 100
DB 241 GCAATGCCGACCTTCTCTTATCAGGATGGCGAAGTGGACACTTGTGCTGGTGGC 300
QY 101 AspGluAspGluLeuArgAspAlaValArgLysTyrAlaAlaAlaGlyThrThrAla 120
DB 301 AGAAGGATGATATCCATACCAAGATA-----GTGGCCCTCATGGTTCTGCATCTGCC 354

RESULT 9

AR414207
LOCUS 466 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 1844 from patent US 6639063.
ACCESSION AR414207
VERSION AR414207.1 GI:40169317
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 466)
AUTHORS Edwards,J.-B.D.M., Jobert,S. and Giordano,J.-Y.
TITLE EST's and encoded human proteins
JOURNAL Patent: US 6639063-A 1844 28-OCT-2003;
FEATURES
source Location/Qualifiers
1. .466
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Alignment Scores:

Score: 2.08e-28 Length: 466
Pred. No.: 315.00 Matches: 67
Percent Similarity: 69.05% Conservative: 20
Best Local Similarity: 53.17% Mismatches: 35
Query Match: 48.31% Indels: 5
DB: 6 Gaps: 1

US-10-005-429-14 (1-126) x AR414207 (1-466)

QY 1 MetAlaAGluGluGluValAlaValIleAlaCysHisThrLysAspGluPheAspAlaArg 20
DB 71 ATGGCGTCGACGACGAGTGGTATCGGTGCCACAGCAGGCTGAGTTCGACGCCAC 130
QY 21 MetAlaLysAlaLysGluGlnGlyLysLeuValValIleAspPheMetAlaProThrCys 40
DB 131 ATGACCAAGGCGCAGAAAGCGCAAGCTGGTGGTGCATCGACTTCACTGCCCGCTGGTGC 190
QY 41 SerGlyCysGlnMetMetAlaProValTyrAlaAspCysAlaSerLysTyrProSerAla 60
DB 191 GT-CCATGCGCGCCCATCGCCCACTGTTGTCGACACGCGCCCAAGATTCTACTAGGTC 249
QY 61 ValPheLeuGluValAspValAspGluLeuLeuGluValAlaLysIleTyrGlyValHis 80
DB 250 GTCTTCTGAAGTGGACGCTGACGAGTGAAGGAAGTCAACCGCGCTTACGAGTCCGAG 309
QY 81 ValMetProThrPheCysPheIleArgAsnGlyGluThrLeuGluSerPheAlaThrVal 100
DB 310 GCGATGCGCGACTTCCACTTGTCAAGAACGCGCAAGCGTCGCGACCATCGTGGTGGC 369
QY 101 AspGluAspGluLeuArgAspAlaValArgLysTyrAlaAlaAlaGlyThrThrAla 120
DB 370 AGGAAGGACGAGCTCTCTGCCCGACGATCGAAGCATCGCGG-----CCTGGC 417
QY 121 ProAlaSerAlaSerAla 126
DB 418 COTGCTCTGCTGCTGCC 435

RESULT 10

BD109760 466 bp DNA linear PAT 18-SEP-2002
LOCUS
DEFINITION EST and encoded human protein.
ACCESSION BD109760
VERSION BD109760.1 GI:23204578
KEYWORDS JP 2002010789-A/1837.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 466)
AUTHORS Edwards,J.B.D.M., Jobert,S. and Giordano,J.E.
TITLE EST and encoded human protein
JOURNAL Patent: JP 2002010789-A 1837 15-JAN-2002;
GENSET CORP
COMMENT OS Homo sapiens (human)
PN JP 2002010789-A/1837
PD 15-JAN-2002
PF 07-AUG-2000 JP 2000280989
PR 05-AUG-1999 US 60/147499
PI JEAN BAPTISTE DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEAN EVE
GIORDANO
PC C12N15/09, C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, PC
C12N1/21,
PC C12N5/10, C12P21/02, C12P21/08, C12Q1/68, C12N15/00, C12N5/00, PC
C12N15/00
CC Von Heijne matrix
CC score 4.30000019073486
CC seq VVIDFTAAVCVHA/AP
CC Location/Qualifiers
FH Key Location/Qualifiers
FT CDS 71..256
FT sig_peptide 71..199.
FT Location/Qualifiers
1. .466

FEATURES

source

```

/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN
Alignment Scores:
Pred. No.: 2.08e-28 Length: 466
Score: 315.00 Matches: 67
Percent Similarity: 69.05% Conservative: 20
Best Local Similarity: 53.17% Mismatches: 35
Query Match: 48.31% Indels: 5
DB: 6 Gaps: 1

US-10-005-429-14 (1-126) x BD109760 (1-466)
Qy 1 MetAlaAlaGluGluGlyAlaValIleAlaCysHisThrLysAspGluPheAspAlaArg 20
Db 71 ATGGCGTCCGAGCGAGGAGTGTGATCGCGCCACAGCAAGGTCGAGTTCGAGCCGAC 130
Qy 21 MetAlaLysAlaLysGluGlnGlyLysLeuValIleAspPheMetAlaProTyrCys 40
Db 131 ATGACCAAGGCCAGAGCGGCGAGCTGTGTGTCGACTTCACCTGCGCGCTGGTGC 190
Qy 41 SerGlyCysGlnMetMetAlaProValTyrAlaAspCysAlaSerLysTyrProSerAla 60
Db 191 GT-CCATCGCGCCATCGCCCACTGTTCGTCGAACACGCGCAAGAGTTCACCTCAGGTC 249
Qy 61 ValPheLeuGluValAspValAspGluLeuGluValAlaLysIleTyrGlyValHis 80
Db 250 GTCTTCGAGGTGAGCTGCGAGAGTGAAGAGTCCACCGCGGCTCAGAGGTGCG 309
Qy 81 ValMetProThrPheCysPheIleArgAsnGlyGluThrLeuGluSerPheAlaThrVal 100
Db 310 GCGATGCGCGACTTCCTCACTTCGTCGAAGCGCAGAGCGTCCGCGCATCGTGGTGCC 369
Qy 101 AspGluAspGluLeuArgAspAlaValArgLysTyrAlaAlaAlaGlyThrThrAla 120
Db 370 AGAAGGACGAGCTCCTGGCCAGATGAGAGCGTCCGCGGCGGCGGCGGCGGCGGCGG 417
Qy 121 ProAlaSerAlaSerAla 126
Db 418 CCTGCTGCTGCTGCTGCC 435

RESULT 11
AY088698 590 bp mRNA linear PLN 14-APR-2003
LOCUS
DEFINITION
Arabidopsis thaliana clone 9219 mRNA, complete sequence.
ACCESSION
AY088698
VERSION
AY088698.1 GI:21407472
KEYWORDS
FLI CDNA.
SOURCE
Arabidopsis thaliana (thale cress)
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 590)
Haas,B.J., Volkovskiy,N., Town,C.D., Trukhan,M., Alexandrov,N.,
Feldmann,K.A., Flavell,R.B., White,O. and Salzberg,S.L.
Full-length messenger RNA sequences greatly improve genome
annotation
JOURNAL
Genome Biol. 3 (6), RESEARCH0029 (2002)
MEDLINE
22088475
PUBMED
12093376
AUTHORS
2 (bases 1 to 590)
Brower,V., Trukhan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and
Feldmann,K.
Full-length cDNA from Arabidopsis thaliana
Unpublished
3 (bases 1 to 590)
Brower,V., Trukhan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and
Feldmann,K.
Direct Submission
Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road,

```

Malibu, CA 90265, USA

This clone sequence is one of 5,000 Ceres full-length cDNAs made available to TIGR and Genbank. The following quality assessment of this set was done by comparison with known proteins: two percent of the clones are estimated to be 5'-truncated; less than one percent are 3'-truncated; approximately two percent represent alternative splice variants, including unspliced introns and spliced exons; one percent may contain premature stop codons; five percent may have frame shifts in a coding region. A sequence is considered to be 5'-truncated if it lacks the translation initiation start (ATG). A sequence is considered to be 3'-truncated if it lacks the C-terminal end of the encoded protein. Please note that these cDNA sequences are derived from the Ws or Laer ecotypes and therefore may contain polymorphisms when compared to sequences from Col-0. Genet carried out the library production and sequencing of the full-length clones. Ceres, Inc. carried out the clustering of the 5' sequences, selection of clones, and sequence assembly.

FEATURES

Location/Qualifiers

1..590

/organism="Arabidopsis thaliana"

/mol_type="mRNA"

/db_xref="taxon:3702"

/clone="9219"

52..411

/codon_start=1

/product="thioredoxin"

/protein_id="AA067018.1"

/db_xref="GI:21617968"

/translation="MAAEQGVISCHTNDVWTVQLDKAKESNKLIVIDFTASCPCCR MIAPINDLAKFMSSAIFPKVDVDELQVAKFGEVEMPTFFVFKAGEVVDKLVNGAN KEDLQAKIVKHTGVTTA"

ORIGIN

Alignment Scores:

Pred. No.: 2.83e-27 Length: 590

Score: 306.50 Matches: 60

Percent Similarity: 68.60% Conservative: 23

Best Local Similarity: 49.59% Mismatches: 35

Query Match: 47.01% Indels: 3

DB: 8 Gaps: 2

US-10-005-429-14 (1-126) x AY088698 (1-590)

Qy 1 MetAlaAlaGluGluGlyAlaValIleAlaCysHisThrLysAspGluPheAspAlaArg 20

Db 52 ATGGCGCGCAGAGGCTCAAGTGTATGTTGTCACAGCAAGCATGATGACGTGCA 111

Qy 21 MetAlaLysAlaLysGluGlnGlyLysLeuValIleAspPheMetAlaProTyrCys 40

Db 112 CTTGATAAGCCCAAGCAATCCAAAGCTGATTGTGATTGATTCATGCTTCATGCTGT 171

Qy 41 SerGlyCysGlnMetMetAlaProValTyrAlaAspCysAlaSerLysTyr--ProSer 59

Db 172 CCACATGCGCGATGATGTCCTCAATTTCAAGATTGGCCAGAGATTCATGTCAGT 231

Qy 60 AlaValPheLeuGluValAspValAspGluLeuGluValAlaLysIleTyrGlyVal 79

Db 232 GCCATCTTCTCAAGGTGGATGTTGATGAATCTCAGAGTGTGCTAAAGAGTTGGTGTG 291

Qy 80 HisValMetProThrPheCysPheIleArgAsnGlyGluThrLeuGluSerPheAlaThr 99

Db 292 GAGCAATGCCAACCTTTGTTTCATTAAAGCCGCGAGAGTGTGGGAATAGCTGTTGGT 351

Qy 100 ValAspGluAspGluLeuArgAspAlaValLargLysTyrAlaAlaGlyThrThrThr 119

Db 352 GCGAATAAGAGATCTTCAGGCGGAATAGTAGGACAT-----ACTGGTGTATCAACT 405

120 Ala 120

406 GCG 408

RESULT 12

AX505469

AX505469	360 bp	DNA	linear	PAT 27-SEP-2002
LOCUS				
DEFINITION	Sequence 164 from Patent WO0216655.			
ACCESSION	AX505469			
VERSION	AX505469.1			
KEYWORDS	Arabidopsis thaliana (thale cress)			
SOURCE	Arabidopsis thaliana			
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.			
REFERENCE	1 Harper J.F., Kreps, J., Wang, X. and Zhu, T.			
AUTHORS	Stress-regulated genes of plants, transgenic plants containing			
TITLE	same, and methods of use			
JOURNAL	Patent: WO 0216655-A 164 28-FEB-2002;			
	(The Scripps Research Institute (US); Syngenta Participations AG			
FEATURES	(CH)			
Source	Location/Qualifiers			
	1..360			
	/organism="Arabidopsis thaliana"			
	/mol_type="unassigned DNA"			
	/db_xref="taxon:3702"			
ORIGIN				
Alignment Scores:				
Pred. No.:	2.11e-27	Length:	360	
Score:	305.50	Matches:	60	
Percent Similarity:	67.77%	Conservative:	22	
Best Local Similarity:	49.59%	Mismatches:	36	
Query Match:	46.86%	Indels:	3	
DB:	6	Gaps:	2	
US-10-005-429-14 (1-126) x AX505469 (1-360)				
QY	1	MetAlaAlaGluGluGlyAlaValIleAlaCysHisThrIleAspGluPheAspAlaArg	20	
DB	1	ATGCGGCGCAGAGAGCGTCAAGTGTGTTGTTCACACGACGATGTATGAGTGTGCA	60	
QY	21	MetAlaLysAlaLysGluGlnGlyLysLeuValIleAspPheMetAlaProTyrCys	40	
DB	61	CTTGATTAAGCCAAAGATCCACAGCTGATGTGATTTGATTTCTGCTTCATGCTGT	120	
QY	41	SerGlyCysGlnMetMetAlaProValTyrAlaAspCysAlaSerLysTyr---	59	
DB	121	CCACCATGGCGCATGATGCTCCAAATTTCAACGATTTGGCCAGAAAGTTCAATGTC	180	
QY	60	AlaValPheLeuGluValAspValAspGluLeuLeuGluValAlaLysIleTyrGlyVal	79	
DB	181	GCCATCTTCTTCAAGTGTGATGTGATGAACATTCAGAGTGTGTGAAGATTTGGTGTG	240	
QY	80	HisValMetProThrPheCysPheIleArgAsnGlyGluThrLeuGluSerPheAlaThr	99	
DB	241	GAGGCAATGCCAACCTTTGTGTTTCATTAAGCGCGGAGATTTGTGGATAAGCTCGT	300	
QY	100	ValAspGluAspGluLeuArgAspAlaValArgLysTyrAlaAlaAlaGlyThrThrThr	119	
DB	301	GCGAATAAAGAGATCTTCAGCGCAAAATAGTGAAGCAT-----ACTGGGTGTACAACT	354	
QY	120	Ala 120		
DB	355	GCG 357		
RESULT 13				
BT004710				
LOCUS	BT004710 360 bp mRNA linear PLN 19-FEB-2003			
DEFINITION	Arabidopsis thaliana At1g19730 gene, complete cds.			
ACCESSION	BT004710			
VERSION	BT004710.1			
KEYWORDS	FLI CDNA.			
SOURCE	Arabidopsis thaliana (thale cress)			
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;			

```

Qy 1 MetAlaAlaGluGluGlyAlaValIleAlaCysHisThrLysAspGluPheAspAlaArg 20
Db 1 ATCGCGGCGAGAGAGGGTCAAGTGTGTTGTTCACACGACGATGTATGAGCTGTGCAA 60
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Qy 21 MetAlaLysAlaLysGluGluGlnGlyValIleAspPheMetAlaProTyrCys 40
Db 61 CTTCGATAAGCGAAGATCCACAGCTGATGTGATTTGATTTCTGCTTCATGCTGT 120
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Qy 41 SerGlyCysGlnMetMetAlaProValTyrAlaAspCysAlaSerLysTyr---ProSer 59
Db 121 CCACCATCCGCGATGATGCTCCAAATTTTCAACGATTTGGCCCAAGAGTTCATGTCAGT 180
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Qy 60 AlaValPheLeuGluValAspValAspGluLeuGluValAlaLysIleTyrGlyVal 79
Db 181 GCCATCTTCTTCAAGTGGATGTGATGAATCTCAGAGTGTGCTAAAGAGCTTTGGGTG 240
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Qy 80 HisValMetProThrPheCysPheIleArgAsnGlyGluThrLeuGluSerPheAlaThr 99
Db 241 GAGGCAATGCCAACCTTTGTTCATTAAAGCCGCGAAGTGTGGATAAGCTCGTTGGT 300
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Qy 100 ValAspGluAspGluLeuArgAspAlaValArgLysTyrAlaAlaGlyThrThr 119
Db 301 CGCAATAAAGAGATCTTCAGCGCAAAATAGTAGAAGCAT-----ACTGGTGTTCACAACT 354
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Qy 120 Ala 120
Db 355 GCG 357

```

```

RESULT 14
LOCUS AK118542
DEFINITION Arabidopsis thaliana At1g19730 mRNA for putative thioredoxin,
complete cds, clone: RAF19-77-A10.
ACCESSION AK118542
VERSION AK118542.1 GI:26452110
KEYWORDS FLI CDNA; CAP trapper.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE
AUTHORS Seki, M., Iida, K., Satou, M., Sakurai, T., Akiyama, K., Ishida, J.,
Nakajima, M., Enju, A., Kamiya, A., Narusaka, M., Carninci, P.,
Kawai, J., Hayashizaki, Y. and Shinozaki, K.
TITLE Arabidopsis thaliana full-length cDNA
JOURNAL Published Only in Database (2002)
AUTHORS 2 (bases 1 to 556)
Seki, M., Iida, K., Satou, M., Sakurai, T., Akiyama, K., Ishida, J.,
Nakajima, M., Enju, A., Kamiya, A., Narusaka, M., Carninci, P.,
Kawai, J., Hayashizaki, Y. and Shinozaki, K.
Direct Submission
Submitted (25-NOV-2002) Motoaki Seki, RIKEN Genomic Sciences
Center; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa
230-0045, Japan (E-mail: msek@gs.c.riken.go.jp,
URL: http://pfweb.gsc.riken.go.jp, Tel: 81-45-503-9625,
Fax: 81-45-503-9586)
COMMENT An Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al. (1998) Plant J. 15:707-720;
Seki et al. (2002) Science 296:141-145). cDNA cleaved with BamHI
and XhoI was ligated to modified Lambda FLC-1-E vector (Carninci et
al. (2001) Genomics 77:79-90) digested with BamHI and SalI.
This clone is in a modified phagescript vector.
Please visit our web site (http://pfweb.gsc.riken.go.jp/) for
further details.
FEATURES
source
1. 556
/organism="Arabidopsis thaliana"
/molecule="mRNA"
/db_xref="Columbia"
/db_xref="taxon:3702"
/chromosome="1"

```

```

/clone="RAF19-77-A10"
/notes="common name: thale cress"
1. 556
/genes="At1g19730/F14P1_32"
23. 382
/genes="At1g19730/F14P1_32"
/codon_start=1
/product="putative thioredoxin"
/protein_id="BAC43145.1"
/db_xref="GI:26452111"
/translation="MAAEEGVIGCHTNDVWTVQLDKAKESNKLIVIDFTASNCPPCR
MTAPIFNDLAKFMSSAIFFKVDVBLQSVAKFEGVEAMFTFFIKAGEYVDLVGAN
KEDLQAKIVKHTGTTTA"
ORIGIN
Alignment Scores:
Pred. No.: 3,49e-27 Length: 556
Score: 305.50 Matches: 60
Percent Similarity: 67.77% Conservative: 22
Best Local Similarity: 49.59% Mismatches: 36
Query Match: 46.86% Indels: 3
DB: 8 Gaps: 2
US-10-005-429-14 (1-126) x AK118542 (1-556)
Qy 1 MetAlaAlaGluGluGlyAlaValIleAlaCysHisThrLysAspGluPheAspAlaArg 20
Db 23 ATCGCGGCGAGAGAGGGTCAAGTGTGTTGTTCACACGACGATGTATGAGCTGTGCAA 82
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Qy 21 MetAlaLysAlaLysGluGlnGlyLysLeuValIleAspPheMetAlaProTyrCys 40
Db 83 CTTCGATAAAGCGAAGATCCCAAGCTGATGTGATTTCTGCTTCATGCTTCATGCTGT 142
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Qy 41 SerGlyCysGlnMetMetAlaProValTyrAlaAspCysAlaSerLysTyr---ProSer 59
Db 143 CCACCATCCGCGATGATGCTCCAAATTTTCAACGATTTGGCCCAAGAGTTCATGTCAGT 202
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Qy 60 AlaValPheLeuGluValAspValAspGluLeuGluValAlaLysIleTyrGlyVal 79
Db 203 GCCATCTTCTTCAAGTGGATGTGATGAATTCAGAGTGTGCTTAAAGAGTGTGCTG 262
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Qy 80 HisValMetProThrPheCysPheIleArgAsnGlyGluThrLeuGluSerPheAlaThr 99
Db 263 GAGGCAATGCCAACCTTTGTGTTCAATTAAGCCGCGAAGTGTGGATAAGCTCGTTGGT 322
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Qy 100 ValAspGluAspGluLeuArgAspAlaValArgLysTyrAlaAlaGlyThrThr 119
Db 323 GCGAATAAAGAGATCTTCAGCGCAAAATAGTAGAAGCAT-----ACTGGTGTTCACAACT 376
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Qy 120 Ala 120
Db 377 GCG 379
RESULT 15
LOCUS ATTHIREDI
DEFINITION A.thaliana (GREN) mRNA for thioredoxin.
ACCESSION Z35473
VERSION Z35473.1 GI:992959
KEYWORDS thioredoxin.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE
AUTHORS Rivera-Madrid, R., Meares, D., Marinho, P., Jacquot, J.P.,
Decottignies, P., Miginiac-Maslow, M. and Meyer, Y.
TITLE Evidence for five divergent thioredoxin h sequences in Arabidopsis
thaliana
JOURNAL PROC. Natl. Acad. Sci. U.S.A. 92 (12), 5620-5624 (1995)
MEDLINE 95296363
PUBMED 7777559

```

REFERENCE 2 (bases 1 to 642)
AUTHORS Meyer, Y.
TITLE Direct Submission
JOURNAL Submitted (22-JUL-1994) Yves Meyer, Labo de Physio et Biol Mol
Vegetales, CNRS, URA 565, Av. de Villeneuve, Perpignan, 66860,
FRANCE

FEATURES
source Location/Qualifiers
1..642
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/db_xref="taxon:3702"
/haplotype="Columbia"
/tissue_type="flower buds"
/dev_stage="early flowering"
41..418
/codon_start=1
/product="thioredoxin"
/protein_id="CAA84610.1"
/db_xref="GI:992960"
/db_xref="GOA:Q39239"
/db_xref="SWISS-PROT:Q39239"
/translation="MAAREGVIGCHTNDVWTVQLDKAKESNKLIVIDFTASNCPPCR
MIAPFNDAIKFMFAIFKVDVDELOSVAKFEGVEAMPTFFVFKAGEVVDKLVGAN
KEDLOAKIVKHTGVTTVNQFEA"

CDS

ORIGIN

Alignment Scores:
Pred. No.: 1.24e-26 Length: 642
Score: 301.50 Matches: 59
Percent Similarity: 67.50% Conservative: 22
Best Local Similarity: 49.17% Mismatches: 36
Query Match: 46.24% Indels: 3
DB: 8 Gaps: 2

US-10-005-429-14 (1-126) x ATTHRED1 (1-642)

Qy 1 MetAlaAlaGluGluGlyAlaValIleAlaCysHisThrLysAspGluPheAspAlaArg 20
Db 41 ATGGCGGCAGAGAGGGTCAAGTGATTGGTTGTACACGACGATGTATGGACTGTGCAA 100
Qy 21 MetAlaLysAlaLysGluGlnGlyLysLeuValValIleAspPheMetAlaProTyrCys 40
Db 101 CITGATAAAGCCAAAGATCCAAACAGCTGATTGTGATTGATTCACCTCTTCATGGTGT 160
Qy 41 SerGlyCysGlnMetMetAlaProValTyrAlaAspCysAlaSerLysTyr---ProSer 59
Db 161 CCACCATGGCGCATGTGCTCCAAATTTCAACGATTTGCCCAAGAGTTTCATGTCAACT 220
Qy 60 AlaValPheLeuGluValAspValAspGluLeuLeuGluValAlaLysIleTyrGlyVal 79
Db 221 GCCATCTTCTCAAGGTGGATGTGATGAACCTTCAGAGTGTGCTAAAGAGTTTGGTGTG 280
Qy 80 HisValMetProThrPheCysPheIleArgAsnGlyGluThrLeuGluSerPheAlaThr 99
Db 281 GAGGCAATGCCACCTTTGTGTTTCATTAAGCCGGCGAAGTTGGATAGCTCGTGTGT 340
Qy 100 ValAspGluAspGluLeuArgAspAlaValArgLysTyrAlaAlaAlaGlyThrThrThr 119
Db 341 GCGAATAAAGAGATCTTCAGGGGGAATAATAGTAGAGCAT-----ACTGGTGTTCACACT 394

Search completed: May 5, 2004, 04:56:23
Job time : 1528.27 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 5, 2004, 00:59:23 ; Search time 162.118 Seconds
(without alignments)

3301.746 Million cell updates/sec

Title: US-10-005-429-14

Perfect score: 652

Sequence: 1 MAEEGAVIACHYKDFDAR.....DAVRKYAAAGTTAPASASA 126

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US10005429/runat_04052004_121648_15427/app_query.fasta_1.782
-DB=N_Geneseq_29Jan04 -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blom62 -TRANS=human40.cgi
-LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=p2n -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10005429 @CNG 1.1 886 @runat_04052004_121648_15427 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_29Jan04.*

1: Geneseq1980s.*
2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001as.*
5: Geneseq2001bs.*
6: Geneseq2002s.*
7: Geneseq2003as.*
8: Geneseq2003bs.*
9: Geneseq2003cs.*
10: Geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	361	55.4	540	9 ADC06863	Adc06863 Plasmid p
2	361	55.4	660	9 ADC06864	Adc06864 Plasmid p
3	361	55.4	686	2 AAQ78205	Aag78205 Gene codi
4	361	55.4	687	3 AAC66375	Aac66375 Rice thlo
5	333	51.1	659	3 ADC06860	Adc06860 Plasmid p
6	306.5	47.0	590	3 AAC38792	Aac38792 Arabidops
7	305.5	46.9	360	6 ABZ12359	Abz12359 Arabidops
8	285	43.7	3888	6 ABN89581	Abn89581 Phaseolin

9	285	43.7	3888	6	ABS53097	AbS53097 DNA encod
10	282.5	43.3	601	3	AAZ51740	Aaz51740 Glycine m
11	282	43.3	345	6	ABZ12358	Abz12358 Arabidops
12	282	43.3	345	6	ABN89587	Abn89587 Arabidops
13	282	43.3	561	3	AAC51522	Aac51522 Arabidops
14	282	43.3	563	3	AAC34121	Aac34121 Arabidops
15	282	43.3	3129	6	ABN89579	Abn89579 Phaseolin
16	282	43.3	3129	6	ABS53095	AbS53095 DNA encod
17	282	43.3	3888	6	ABN89580	Abn89580 Phaseolin
18	282	43.3	3888	6	ABS53096	AbS53096 DNA encod
19	279	42.8	470	3	AAC37781	Aac37781 Arabidops
20	275	42.2	738	3	AAZ51739	Aaz51739 Glycine m
21	275	42.2	4935	6	ABN89586	Abn89586 Promoter-
22	267	41.0	509	5	AAH87768	Aah87768 Peppermin
23	265	40.6	574	3	AAZ51738	Aaz51738 Catalpa s
24	261	40.0	653	2	AAQ99783	Aaq99783 Plant SAR
25	261	40.0	653	2	AAV62799	Aav62799 Tobacco S
26	261	40.0	653	2	AAV81683	Aav81683 Tobacco p
27	260	39.9	614	3	AAZ51741	Aaz51741 Vernonia
28	260	39.9	870	3	AAZ51737	Aaz51737 Momordica
29	254	39.0	366	7	ADA70643	Ada70643 Rice gene
30	253	38.8	393	2	AAT10451	Aat10451 Hard whea
31	253	38.8	393	2	AAC62457	Aac62457 Wheat thi
32	253	38.8	560	3	AAC41961	Aac41961 Arabidops
33	252.5	38.7	524	3	AAC33829	Aac33829 Arabidops
34	252	38.7	320	3	AAZ31785	Aaz31785 Plant mic
35	252	38.7	328	3	AAZ31097	Aaz31097 Plant mic
36	252	38.7	357	6	ABZ13931	Abz13931 Arabidops
37	252	38.7	357	7	ADA67904	Ada67904 Arabidops
38	252	38.7	480	3	AAC36542	Aac36542 Arabidops
39	252	38.7	563	3	AAC34211	Aac34211 Arabidops
40	252	38.7	576	7	ABX56868	Abx56868 Arabidops
41	252	38.7	652	3	AAC48656	Aac48656 Arabidops
42	251	38.5	369	3	AAC61537	Aac61537 Nucleotid
43	251	38.5	369	9	AAU59629	Aau59629 Barley th
44	249	38.2	382	3	AAC62456	Aac62456 Wheat thi
45	249	38.2	384	2	AAT10450	Aat10450 Soft whea

ALIGNMENTS

RESULT 1

ADC06863

ID ADC06863 standard; DNA; 540 BP.

XX

AC ADC06863;

XX

DT 18-DEC-2003 (first entry)

XX

DE Plasmid pDONR201 containing the modified rice thioedoxin H DNA.

XX

XX cloning; recombination method; ds; plasmid pDONR201; rice; thioedoxin H.

OS Synthetic.

OS Unidentified.

OS Oryza sativa.

XX

PN US2003143618-A1.

XX

PD 31-JUL-2003.

XX

PF 23-JAN-2003; 2003US-00349782.

XX

PR 23-JAN-2002; 2002EP-00075373.

XX

PA (HATZ/) HATZFIELD Y.

PA (FRAN/) FRANKARD V M.

XX (DROU/) DROUAL A.

PI Hatzfield Y, Frankard VM, Droual A;

XX WPI; 2003-671205/63.

DR

XX

PT Producing a modified, chimeric, or reconstructed DNA molecule of two
 PT parts comprising amplifying the two DNAs by PCR using primers
 PT incorporating recombination sites, ligating the PCR products, and then
 PT cloning the ligated products.

PS Disclosure; Fig 5; 15pp; English.

CC The invention relates to a novel method for producing a modified,
 CC chimeric, or reconstructed DNA molecule composed of 2 parts. The method
 CC comprises PCR amplification of each part using two primer sets that build
 CC in recombination sites at the outer ends of each PCR product, ligating
 CC the two PCR products and cloning the ligated products into a
 CC recombination vector. The method of the invention may be useful for the
 CC easy cloning and selection of chimeric DNA molecules. Unlike classical
 CC recombination methods the new method avoids the need for initial cloning
 CC using restriction enzymes and allows the production of mutated and/or
 CC chimeric DNA molecules. The current sequence is that of the plasmid
 CC pDONR201 of the invention which contains the modified rice thioredoxin H
 CC DNA.

SQ Sequence 540 BP; 144 A; 130 C; 135 G; 131 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 4.2e-40 Length: 540
 Score: 361.00 Matches: 70
 Percent Similarity: 71.77% Conservative: 19
 Best Local Similarity: 56.45% Mismatches: 33
 Query Match: 55.37% Indels: 2
 DB: 9 Gaps: 1

US-10-005-429-14 (1-126) x ADC06863 (1-540)

Qy 1 MetAlaAlaGluGluGlyAlaValIleAlaCysHisThrLysAspGluPheAspAlaArg 20
 Db 58 ATGGCGCGCGAGGAGGAGTGTGATCGCTGCCACCAAGGACGAGTTCGAGCCCGAG 117
 Qy 21 MetAlaLysAlaLysGluGlnGlyLysLeuValIleAspPheMetAlaProTyrCys 40
 Db 118 ATGACCAAGGCCAGGAGCGCGCAAGTGGTCATAATTCAGTTCCTCTGCTGTC 177
 Qy 41 SerGlyCysGlnMetMetAlaProValTyrAlaAspCysAlaSerLysTyrProSerAla 60
 Db 178 GGACGTCGCGCTTCATCGCCCGAGTGTGCTGAATACGCCAAAAGTTCCTCTGCTGCT 237
 Qy 61 ValPheLeuGluValAspValAspGluLeuGluValAlaLysIleTyrGlyValHis 80
 Db 238 GTCTTCCTGAAGGTTGATGTTGATGAGCTGAAGGAAGTGTGCTGAAGGATCAATGTCGAG 297
 Qy 81 ValMetProThrPheCysPheIleArgAsnGlyGluThrLeuGluSerPheAlaThrVal 100
 Db 298 GCAATGCCGACCTTCTTATTCATCAAGGATGCTGAGGCTGACCAAGTCTGTCGCC 357
 Qy 101 AspGluAspGluLeuArgAspAlaValArgLysTyrAlaAlaGlyThrThrAla 120
 Db 358 AGGAAGGATGACCTCCAGAACCACTGCTGAGGAC-----GTCCGTGCCACTGCTGCA 411
 Qy 121 PrcAlaSerAla 124
 Db 412 TCTGCTTCGCC 423

RESULT 2

ADC06864
 ID ADC06864 standard; DNA; 660 BP.

AC ADC06864;

XX 18-DEC-2003 (first entry)

DE Plasmid pDONR201 containing the rice thioredoxin H DNA - alternative.
 DE cloning; recombination method; ds; plasmid pDONR201; rice; thioredoxin H.
 XX Unidentified.

OS Oryza sativa.
 XX US2003143618-A1.
 XX 31-JUL-2003.
 XX 23-JAN-2003; 2003US-00349782.
 XX 23-JAN-2002; 2002EP-00075373.
 XX (HATZ/) HATZFIELD Y.
 XX (FRAN/) FRANKARD V M.
 XX (DROU/) DROUAL A.
 PI Hatzfield Y, Frankard VM, Droual A;
 DR WPI; 2003-671205/63.
 XX Producing a modified, chimeric, or reconstructed DNA molecule of two
 PT parts comprising amplifying the two DNAs by PCR using primers
 PT incorporating recombination sites, ligating the PCR products, and then
 PT cloning the ligated products.

Disclosure; Fig 2; 15pp; English.

CC The invention relates to a novel method for producing a modified,
 CC chimeric, or reconstructed DNA molecule composed of 2 parts. The method
 CC comprises PCR amplification of each part using two primer sets that build
 CC in recombination sites at the outer ends of each PCR product, ligating
 CC the two PCR products and cloning the ligated products into a
 CC recombination vector. The method of the invention may be useful for the
 CC easy cloning and selection of chimeric DNA molecules. Unlike classical
 CC recombination methods the new method avoids the need for initial cloning
 CC using restriction enzymes and allows the production of mutated and/or
 CC chimeric DNA molecules. The current sequence is that of the plasmid
 CC pDONR201 of the invention which contains the rice thioredoxin H DNA. This
 CC sequence, located in figure 2, differs from that in the sequence listing.

SQ Sequence 660 BP; 172 A; 160 C; 159 G; 169 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 5.6e-40 Length: 660
 Score: 361.00 Matches: 70
 Percent Similarity: 71.77% Conservative: 19
 Best Local Similarity: 56.45% Mismatches: 33
 Query Match: 55.37% Indels: 2
 DB: 9 Gaps: 1

US-10-005-429-14 (1-126) x ADC06864 (1-660)

Qy 1 MetAlaAlaGluGluGlyAlaValIleAlaCysHisThrLysAspGluPheAspAlaArg 20
 Db 130 ATGCGCGCGAGGAGGAGTGTGATCGCTGCCACCAAGGACGAGTTCGAGCCCGAG 189
 Qy 21 MetAlaLysAlaLysGluGlnGlyLysLeuValIleAspPheMetAlaProTyrCys 40
 Db 190 ATGACCAAGGCCAGGAGCGCGCAAGTGGTCATAATTCAGTTCCTCTGCTGCT 249
 Qy 41 SerGlyCysGlnMetMetAlaProValTyrAlaAspCysAlaSerLysTyrProSerAla 60
 Db 250 GGCCCTTCGCGCTTCATCGCCCGAGTGTGCTGAATACGCCAAAAGTTCCTCTGCTGCT 309
 Qy 61 ValPheLeuGluValAspValAspGluLeuGluValAlaLysIleTyrGlyValHis 80
 Db 310 GTCTTCCTGAAGGTTGATGTTGATGAGCTGAAGGAGTGTGCTGAAGGATCAATGTCGAG 369
 Qy 81 ValMetProThrPheCysPheIleArgAsnGlyGluThrLeuGluSerPheAlaThrVal 100
 Db 370 GCAATGCCGACCTTCTTATTCATCAAGGATGCTGAGGCTGACCAAGTCTGTCGCCGCC 429
 Qy 101 AspGluAspGluLeuArgAspAlaValArgLysTyrAlaAlaGlyThrThrAla 120
 Db 430 AGGAAGGATGACCTCCAGAACCACTGCTGAGGAC-----GTCCGTGCCACTGCTGCA 483

QY	121 ProAlaSerAla 124
Df	484 TCTGCTTCGCC 495
RESULT 3	
ID	AAQ78205
XX	AAQ78205 standard; cDNA; 686 BP.
XX	AAQ78205;
DT	16-OCT-2003 (revised)
DT	13-JUL-1995 (first entry)
DE	Gene coding for protein found in phloem sieve tube of rice.
XX	Phloem sieve tube element; plant vascular bundle; rice;
KW	protein transport; migration; fusion protein; ds.
XX	Oryza sativa; (var. aichiasahi).
OS	
Key	Location/Qualifiers
5'UTR	1..56
FT	/tag= b
CDS	57..425
FT	/tag= a
3'UTR	426..686
FT	/tag= c
PN	JP06269286-A.
PD	27-SEP-1994.
PF	19-MAR-1993; 93JP-00060763.
PP	19-MAR-1993; 93JP-00060763.
PR	(MITS-) MITSUI GYOSAI SHOKUBUTSU BIO KENKYUSHO.
PA	WPI; 1994-346185/43.
DR	P-PSDB; AAR65908.
XX	Plant sieve tube protein gene - useful for transfer of useful proteins to the sieve tube.
PT	Claim 1; Page 6; 13pp; Japanese.
PS	Proteins obtained from the proboscis of a rice leaf hopper (Nilaparvata lugens Stal) were analysed; AAR65909 is the partial sequence of a fragment of a protein that is transported to the sieve tube. Based on this partial amino acid sequence, a probe (AAQ78206) was designed to screen for a sequence coding for the protein. A gene was cloned from the "aichiasahi" variety of rice (AAQ78205). By fusing the gene to a sequence coding for a second useful protein, the second protein will be transported to the sieve tube. (Updated on 16-OCT-2003 to standardise OS field)
XX	Sequence 686 BP; 170 A; 150 C; 182 G; 184 T; 0 U; 0 Other;
SQ	
Alignment Scores:	
Pred. No.:	5,928-40 Length: 686
Score:	361.00 Matches: 70
Percent Similarity:	71.7% Conservative: 19
Best Local Similarity:	56.4% Mismatches: 33
Query Match:	55.3% Indels: 2
DB:	2 Gaps: 1
US-10-005-428-14 (1-126) x AAQ78205 (1-686)	
QY	1 MetalAlaGluGlnGlyValAlaValIleAspPheMetAlaProThrCys 20
Df	57 ATGGCGCCGAGGAGGTCTGATCGCTGCCACACAGGAGCGATTCTGCAGCCGAC 116
US-10-005-428-14 (1-126) x AAQ78205 (1-686)	
QY	1 MetalAlaLysAlaLysGluGlnGlyValAlaValIleAspPheMetAlaProThrCys 40
Df	117 ATGACCAAGGCGAAGGAGCGCGCAAGTGTCTATAATTGACTTCACTGCTTCTCGTG 176
QY	41 SerGlyCysGlnMetMetAlaProValTyraAlaAspCysAlaSerLysTyrProSerAla 60
Df	177 GGCCCTTGGCGTTTCATCCGCCAGTGTTCGCTGAATACGCCAAAAGTTCCCTGTGCT 236
QY	61 ValPheLeuGluValAlaAspValAspGluLeuLeuGluValAlaLysIleTyrGlyValHis 80
Df	237 GTCTTCTCTGAAGGTGTGATGTGATGAGCTGAAGGAAGTTGCTGAAGAAGTACAATGTGAG 296
QY	81 ValMetProThrPheCysPheIleArgAsnGlyGluThrLeuGluSerPheAlaThrVal 100
Df	297 GCAATGCCGACCTCTCTATTCAAGGATGGTCTGAGGCTGACAGGTCGTGGCGCC 356
QY	101 AspGluAspGluLeuArgAspAlaValAlaGlyTyrAlaAlaIleGlyThrThrAla 120
Df	357 AGGAAGGATGACCTCCAGAACACCACCATGCTGAAGCAC-----GTGGGTGCCACTGCTGCA 411
QY	121 ProAlaSerAla 124
Df	411 TCTGCTTCGCC 422
RESULT 4	
ID	AAC66375 standard; cDNA; 687 BP.
XX	AAC66375;
XX	23-FEB-2001 (first entry)
XX	Rice thioredoxin h cDNA sequence.
XX	Transformed plant; transfer protein; intercellular transfer;
XW	thioredoxin h; rice; ss.
XX	Oryza sativa.
XX	Key
PH	Location/Qualifiers
FT	57..425
FT	/tag= a
FT	/product= "Thioredoxin h"
XX	JP20000262169-A.
XX	26-SEP-2000.
XX	19-MAR-1999; 99JP-00074914.
XX	19-MAR-1999; 99JP-00074914.
XX	(KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX	WPI; 2000-682116/67.
DR	P-PSDB; AAB35810.
XX	Transformed plants which can control the intercellular transfer of molecules using protoplasmic connections.
PT	Example; Page 6-7; 8pp; Japanese.
PS	This invention relates to a method for the production of a transformed plant which contains DNA which hybridises with DNA encoding a transfer protein. The transformed plant can control the intercellular transfer of a substance through the protoplasmic connections in the plant. The present sequence represents cDNA encoding rice thioredoxin h. The cDNA sequence is used in an example illustrating the method of the invention
XX	Sequence 687 BP; 171 A; 150 C; 182 G; 184 T; 0 U; 0 Other;
SQ	
Alignment Scores:	
Pred. No.:	5,936-40 Length: 687

Score: 361.00 Matches: 70
Percent Similarity: 71.77% Conservative: 19
Best Local Similarity: 56.45% Mismatches: 33
Query Match: 55.37% Indels: 2
DB: 3 Gaps: 1

US-10-005-429-14 (1-126) x AAC66375 (1-687)

QY 1 MetAlaAlaGluGluGlyAlaValIleAlaCysHisThrLysAspGluPheAspAlaArg 20
Db 57 ATGGCGCGGAGGAGGAGTCTGATCGCTCCCAACAAAGGAGGAGTTCGACCCGAG 116
QY 21 MetAlaLysAlaLysGluGluGlyLysLeuValIleAspPheMetAlaProTyrCys 40
Db 117 ATGACCAAGCCAGGAGGCGGCAAGGTCATATGACTTCAGTCTCTCTGCTGT 176

QY 41 SerGlyCysGlnMetAlaProValTyrAlaAspCysAlaSerIleTyrProSerAla 60
Db 177 GGCCTTGGCTTATCGCCCGGAGTTCGCTGATAGCCCAAAAAGTTCCTGCTGT 236

QY 61 ValPheLeuGluValAspValAspGluLeuValAlaLysIleTyrGlyValHis 80
Db 237 GCTCTCTGAGGTTGATGTTGATGAGCTGAAGGAGTTCCTGAAAAGTACATGTCGAG 296

QY 81 ValMetProThrPheCysPheIleArgAsnGlyGluThrLeuGluSerPheAlaThrVal 100
Db 297 GCAATGCCGACCTTCTATTCTCAAGGATGCTGCTGAGGCTGACAAAGGCTGTCGCGCC 356

QY 101 AspGluAspGluLeuValAspValAlaValArgIleTyrAlaAlaGlyThrThrAla 120
Db 357 AGGAAGGATGACCTCCAGAACACCATCTGTAAGGAC-----GTCGGTGCCACTGCTGCA 410

QY 121 ProAlaSerAla 124
Db 411 TCTGCTTCTGCC 422

RESULT 5
ADC06860
ID ADC06860 standard; DNA; 659 BP.
XX AC ADC06860;
XX AC
XX DT 18-DEC-2003 (first entry)
XX DE Plasmid pDONR201 containing the rice thioresdoxin H DNA.
XX DE cloning; recombination method; ds; plasmid pDONR201; rice; thioresdoxin H.
XX OS Unidentified.
XX OS Oryza sativa.
XX PN US2003143618-A1.
XX PD 31-JUL-2003.
XX PF 23-JAN-2003; 2003US-00349782.
XX PR 23-JAN-2002; 2002EP-00075373.
XX (HATZ/) HATZFIELD Y.
XX (FRAN/) FRANKARD V M.
XX (DROU/) DROUAL A.
XX Hatzfield Y, Frankard VM, Droual A;
XX WPI; 2003-671205/63.
XX Producing a modified, chimeric, or reconstructed DNA molecule of two
XX parts comprises amplifying the two DNAs by PCR using primers
XX incorporating recombination sites, ligating the PCR products, and then
XX cloning the ligated products.
XX Disclosure; Page 7; 15pp; English.

XX The invention relates to a novel method for producing a modified,
CC chimeric, or reconstructed DNA molecule composed of 2 parts. The method
CC comprises PCR amplification of each part using two primer sets that build
CC in recombination sites at the outer ends of each PCR product, ligating
CC the two PCR products and cloning the ligated products into a
CC recombination vector. The method of the invention may be useful for the
CC easy cloning and selection of chimeric DNA molecules. Unlike classical
CC recombination methods the new method avoids the need for initial cloning
CC using restriction enzymes and allows the production of mutated and/or
CC chimeric DNA molecules. The current sequence is that of the plasmid
CC pDONR201 of the invention which contains the rice thioresdoxin H DNA.
XX SQ Sequence 659 BP; 172 A; 159 C; 159 G; 169 T; 0 U; 0 Other;

Alignment Scores:
Pzed. No.: 4.16e-36 Length: 659
Score: 333.00 Matches: 69
Percent Similarity: 70.97% Conservative: 19
Best Local Similarity: 55.65% Mismatches: 34
Query Match: 51.07% Indels: 3
DB: 9 Gaps: 1

US-10-005-429-14 (1-126) x ADC06860 (1-659)

QY 1 MetAlaAlaGluGluGlyAlaValIleAlaCysHisThrLysAspGluPheAspAlaArg 20
Db 130 ATGGCGCGGAGGAGGAGTCTGATCGCTCCCAACAAAGGAGGAGTTCGACCCGAG 189

QY 21 MetAlaLysAlaLysGluGluGlyLysLeuValIleAspPheMetAlaProTyrCys 40
Db 190 ATGACCAAGCCAGGAGGCGGCAAGGTCATATGACTTCAGTCTCTCTGCTGT 249

QY 41 SerGlyCysGlnMetAlaProValTyrAlaAspCysAlaSerIleTyrProSerAla 60
Db 250 GGCCTTGGCTTATCGCCCGGAGTTCGCTGATAGCCCAAAAAGTTCCTGCTGT 309

QY 61 ValPheLeuGluValAspValAspGluLeuValAlaLysIleTyrGlyValHis 80
Db 310 GTCTTCTCTGAGGTTGATGTTGATGAGCTGAAGGAGTTCGTAAGTACATGTCGAG 369

QY 81 ValMetProThrPheCysPheIleArgAsnGlyGluThrLeuGluSerPheAlaThrVal 100
Db 370 GCAATGCCGACCTTCTCTATTCTCAAGGATGCTGCTGAGGCTGACAAAGGCTGTCGCGCC 428

QY 101 AspGluAspGluLeuValAspValAlaValArgIleTyrAlaAlaGlyThrThrAla 120
Db 429 AGGAAGGATGACCTCCAGAACACCATCTGTAAGGAC-----GTCGGTGCCACTGCTGCA 482

QY 121 ProAlaSerAla 124
Db 483 TCTGCTTCTGCC 494

RESULT 6
AAC38792
ID AAC38792 standard; DNA; 590 BP.
XX AC AAC38792;
XX AC
XX DT 17-OCT-2000 (first entry)
XX DE Arabidopsis thaliana DNA fragment SEQ ID NO: 22248.
XX OS Arabidopsis thaliana.
XX EP1033405-A2.
XX 06-SEP-2000.
XX

XX Hybridisation assay; genetic mapping; gene expression control;
XX protein identification; signal transduction pathway; metabolic pathway;
XX promoter; termination sequence; 5S.

PF 25-FEB-2000; 2000EP-00301439.
XX 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123130P.
PR 08-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 01-APR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 08-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 24-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 07-MAY-1999; 99US-0132487P.
PR 11-MAY-1999; 99US-0132863P.
PR 14-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 18-MAY-1999; 99US-0134370P.
PR 19-MAY-1999; 99US-0134768P.
PR 20-MAY-1999; 99US-0134941P.
PR 21-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 25-MAY-1999; 99US-0135629P.
PR 27-MAY-1999; 99US-0136021P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139452P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139753P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140993P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 05-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 06-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 08-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 13-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149802P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.

Db 121 CCACCATGCGCGATGATGTCCTCAATTTTCAACGATTGGCCAAAGTTGATGTCAGTCAAGT 180
Qy 60 AlaValPheLeuGluValAspValAspGluLeuLeuGluValAlaLysIleTyrGlyVal 79
Db 181 GCAATCTTCTTCAAGTGGATGTTGATGAACTTCAGAGTGTGCTAAAGAGTTTGGTGTG 240
Qy 80 HisValMetProThrPheCysPheIleArgAsnGlyGluThrLeuGluSerPheAlaThr 99
Db 241 GAGCAATGCCAACCTTGTGTTCTTCAATAAGCCGCGAAGTTGGGATAAGCTCGTTGGT 300
Qy 100 ValAspGluLeuGluValAspValAlaValArgLysTyrValAlaAlaGlyThrThr 119
Db 301 CGGATAAAGAGATCTTCAGCGAAATAGTGAAGCAT-----ACTGGTGTACACT 354
Qy 120 Ala 120
Db 355 GCG 357
RESULT 8
ABN89581
ID ABN89581 standard; DNA; 3888 BP.
XX AC
XX ABN89581;
XX DT 06-SEP-2002 (first entry)
XX DE Phaseolin promoter-Trxh oleosin-phaseolin terminator DNA SEQ:19.
XX KW Multimeric protein; redox protein; thiorodoxin; thiorodoxin reductase;
XX KW oil body; ophthalmological; antidiabetic; cytostatic; antipsoriatic;
XX KW vasotrophic; vulnery; antibacterial; immunosuppressive; antiulcer;
XX KW food product; milk; wheat; oxidative stress; cataract; diabetes;
XX KW chronic obstructive pulmonary disease; envenomation; psoriasis; sepsis;
XX KW bronchiolopulmonary disease; malignancy; reperfusion injury; wound healing;
XX KW gastro intestinal bleeding; intestinal bowel disease; ulcer;
XX KW gastro oesophageal reflux disease; gene; ds.
XX OS Arabidopsis sp.
XX OS Phaseolus vulgaris.
XX PN WO2000250289-A1.
XX PD 27-JUN-2002.
XX PF 19-DEC-2001; 2001WO-US050240.
XX PR 19-DEC-2000; 2000US-00742900.
XX PR 05-JUL-2001; 2001US-0302885P.
XX PR 04-DEC-2001; 2001US-00006038.
XX PA (SEWB-) SEMBIOSYS GENETICS INC.
XX PA (SYGN) SYNGENTA PARTICIPATIONS AG.
XX PI Van Rooijen G, Deckers H, Heifetz PB, Briggs SP, Dalmia BK;
PI Del Val G, Zaplachinski S, Moloney M;
XX DR WPI; 2002-508806/54.
XX DR P-PSDB; ABP60683.
XX PT Producing oil body associated with recombinant multimeric protein complex
XX PT e.g. redox proteins and immunoglobulins comprises producing recombinant
XX PT polypeptides capable of forming the complex in cells comprising oil
XX PT bodies.
XX PS Example 2; Page 169-171; 362pp; English.
XX CC The present invention describes a method (M1) for producing an oil body
XX CC associated with a recombinant multimeric protein complex (MPC). M1
XX CC comprises producing in a cell comprising oil bodies a first and second
XX CC recombinant polypeptide (P1, P2), where P1 is capable of associating with
XX CC P2 to form the MPC and associating the complex with an occlusion body
XX CC (OB) through an OB-targeting-protein capable of associating with OB and
XX CC P1. M1 is useful for producing an oil body associated with a recombinant

CC MPC. The oil bodies are further formulated for use in the preparation of
CC a food product such as milk or wheat based food product, personal care
CC product which reduces the oxidative stress on the surface area of the
CC human body or used to lighten the skin, or a pharmaceutical composition
CC used to treat chronic obstructive pulmonary disease (COPD), cataracts,
CC diabetes, envenomation, bronchiolopulmonary disease, psoriasis,
CC malignancies, reperfusion injury, wound healing, sepsis, gastro
CC intestinal (GI) bleeding, intestinal bowel disease (IBD), ulcers, GERD
CC (gastro oesophageal reflux disease). ABN89589 to ABN89593 and ABP60677 to
CC ABP60964 represent sequence given in the exemplification of the present
CC invention
XX SQ Sequence 3888 BP; 1254 A; 722 C; 613 G; 1299 T; 0 U; 0 Other;
Alignment Scores: 2.33e-28 Length: 3888
Pred. No.: 285.00 Matches: 52
Score: 63.56% Conservative: 23
Percent Similarity: 44.07% Mismatches: 43
Best Local Similarity: 43.71% Indels: 0
Query Match: 6 Gaps: 0
DB:
US-10-005-429-14 (1-126) x ABN89581 (1-3888)
Qy 1 MetAlaAlaGluGluGlyAlaValIleAlaCysHisThrLysAspGluPheAspAlaArg 20
Db 1555 ATGGCTCGGAGAGAGGACAAAGTGATCGCTGCCACACCGTTGAGACATGGACGAGCAG 1614
Qy 21 MetAlaLysAlaLysGluGluGlyLysLeuValIleAspPheMetAlaProTyrCys 40
Db 1615 CTTCAGAAAGCTAATGAATCAAAACCTCTTGTGTGTTGATTTTCAGCGGCTCTTGTGTG 1674
Qy 41 SerGlyCysGlnMetMetAlaProValTyrAlaAspCysAlaSerLysTyrProSerAla 60
Db 1675 GGACCATGCTGTTTCATCGCTCCATCTTCTGCTGATTGGCTAAGAACTTCCTAACGTG 1734
Qy 61 ValPheLeuGluValAspValAspGluLeuLeuGluValAlaLysIleTyrGlyValHis 80
Db 1735 CTTTTCTCAAGGTTCATCTACTGATGATTAATGAAGTTCGGTGGCAAGTCAATGGCGATACAG 1794
Qy 81 ValMetProThrPheCysPheIleArgAsnGlyGluThrLeuGluSerPheAlaThrVal 100
Db 1795 GCGATGCCAACCTTCATGTTTGAAGGAGGAGGAGATTTTGGACAAAGTTGTGGAGCC 1854
Qy 101 AspGluAspGluLeuArgAspAlaValArgLysTyrAlaAlaLysIleTyrThr 118
Db 1855 AAGAAAGATGAGCTTCAGTCTACCATTTGCCAACACTTGGCTATGGCGGATACA 1908
RESULT 9
ABN53097
ID ABN53097 standard; DNA; 3888 BP.
XX AC ABN53097;
XX DT 29-NOV-2002 (first entry)
XX DE DNA encoding Thiorodoxin-oleosin fusion protein.
XX KW Thiorodoxin; thiorodoxin reductase; gene expression; oleosin; oil body;
XX KW oleosin-thiorodoxin fusion protein; gene; ds.
XX OS Arabidopsis thaliana.
XX OS Brassica napus.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX CDS 1555..2658
XX FT /*tag= a
XX FT /product= "Thiorodoxin-oleosin fusion protein"
XX FT 1555..2250
XX FT /*tag= b
XX FT /number= 1
XX FT 2251..2489
XX FT intron


```

PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 28-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 02-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 08-JUL-1999; 99US-0142300P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144335P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 23-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149923P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.

PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 13-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 28-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 18-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161599P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161922P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Alignment Scores:
Pred. No.: 3,72e-29
Score: 282.00
Percent Similarity: 64.91%
Best Local Similarity: 44.74%
Query Match: 43.25%
DB: 3

US-10-005-429-14 (1-126) x AAC51522 (1-561)

Qy 1 MetAlaAlaGluGlyAlaValIleAlaCysHisThrLysAspGluPheAspAlaArg 20
Db 94 ATGGCTTCGGAAGAGGACAGTATCGCTGCCACCGTTGAGACATGGACGAGCAG 153
Qy 21 MetAlaLysAlaLysGluGlnGlyLysLeuValValIleAspPheMetAlaProTyrCys 40
Db 154 CTTTCAGAGGCTTAATGAATCCAAACTCTTTGTGGTGGTATTTCACGGCTTCTTGTGTGT 213
Qy 41 SerGlyCysGlnMetMetAlaProValTyrAlaAspCysAlaSerLysTyrProSerAla 60
Db 214 GGACCATGTGCTTTCATCGCTCCATCTTCTTGTGATTGCTTAAGAACTTCCTAAGCTG 273

```

```

QY 61 ValPheLeuGluValAspValAspGluLeuLeuGluValAlaLysIleTyrGlyValHis 80
DB 274 CTTTCCTCAAGGTGATGACTGATGATGAAGTCGGTGGCAGTATGGCCGATACAG 333
QY 81 ValMetProThrPheCysPheIleArgSnglyGluThrLeuGluSerPheAlaThrVal 100
DB 334 GCGATGCCAACCTTCATGTTTTGAAGGAAGGAAGATTTTGGACAAAGTTGTTGGAGCC 393
QY 101 AspGluAspGluLeuArgAspAlaValAlaGlyTyrAlaAla 114
DB 394 AAGAAGATGACCTTCAGTCTACCATTCACCAACACTTGCT 435

RESULT 14
AAC34121
ID AAC34121 standard; DNA; 563 BP.
XX
AC AAC34121;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 5524.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-00301439.
XX
PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 03-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 29-MAR-1999; 99US-0126264P.
PR 01-APR-1999; 99US-0126785P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 28-APR-1999; 99US-0130891P.
PR 30-APR-1999; 99US-0131449P.
PR 04-MAY-1999; 99US-0132407P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139432P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 02-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.

```


PT e.g. redox proteins and immunoglobulins comprises producing recombinant
PT polypeptides capable of forming the complex in cells comprising oil
XX bodies.
XX
PS Example 2; Page 165-166; 362pp; English.
XX
XX The present invention describes a method (M1) for producing an oil body
CC associated with a recombinant multimeric protein complex (MPC). M1
CC comprises producing in a cell comprising oil bodies a first and second
CC recombinant polypeptide (P1, P2), where P1 is capable of associating with
CC P2 to form the MPC and associating the complex with an occlusion body
CC (OB) through an OB-targeting-protein capable of associating with OB and
CC P1. M1 is useful for producing an oil body associated with a recombinant
CC MPC. The oil bodies are further formulated for use in the preparation of
CC a food product such as milk or wheat based food product, personal care
CC product which reduces the oxidative stress on the surface area of the
CC human body or used to lighten the skin, or a pharmaceutical composition
CC used to treat chronic obstructive pulmonary disease (COPD), cataracts,
CC diabetes, envenomation, bronchiopulmonary disease, psoriasis,
CC malignancies, reperfusion injury, wound healing, sepsis, gastro
CC intestinal (GI) bleeding, intestinal bowel disease (IBD), ulcers, GERD
CC (gastro oesophageal reflux disease). ABN89569 to ABN89593 and ABP60677 to
CC ABP60964 represent sequence given in the exemplification of the present
CC invention
XX
SQ Sequence 3129 BP; 1051 A; 549 C; 439 G; 1090 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	4,42e-28	Length:	3129
Score:	282.00	Matches:	51
Percent Similarity:	64.91%	Conservative:	23
Best Local Similarity:	44.74%	Mismatches:	40
Query Match:	43.25%	Indels:	0
DB:	6	Gaps:	0

US-10-005-429-14 (1-126) x ABN89579 (1-3129)

QY	1	MetAlaAlaGluGluGlyAlaValIleAlaCysHisThrLysAspGluPheAspAlaArg	20
Db	1555	ATGGCTTCGGAGAGACAGATGTCGCTGCCACACGTTGAGACATGGAACGAGCAG	1614
QY	21	MetAlaLysAlaLysGluGlnGlyLysLeuValValIleAspPheMetAlaProTrpCys	40
Db	1615	CTTCAGAGGCTAAATGAATCCAAACTCTGTGGTGGTTGATTTCACGGCTTCTGGTGT	1674
QY	41	SerGlyCysGlnMetMetAlaProValTyrAlaAspCysAlaSerLysTyrProSerAla	60
Db	1675	GGACCATGCGTTCATCGCTTCATCTTTGCTGATTGGCTAAGAACTTCTTAACGTG	1734
QY	61	ValPheLeuGluValAspValAspGluLeuLeuGluValAlaLysIleTyrGlyValHis	80
Db	1735	CTTTTCTCAAGTTGATCTGATGAATTCAGTCGTCGTCGTCGTCGTCGTCGTCGTCG	1794
QY	81	ValMetProThrPheCysPheIleArgAscGlyGluThrLeuGluSerPheAlaThrVal	100
Db	1795	GGCATGCCAACCCTTCATGTTTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	1854
QY	101	AspGluAspGluLeuArgAspAlaValArgLysTyrAlaAla	114
Db	1855	AAGAAAGATGAGCTTCAGTCTACCATTCACCAACACTTCGCT	1896

Search completed: May 5, 2004, 03:24:14
Job time : 170.118 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 5, 2004, 03:03:23 ; Search time 1168.74 Seconds
(without alignments)
3219.395 Million cell updates/sec

Title: US-10-005-429-14
Perfect score: 652
Sequence: 1 MAEEGAVIACHTDEFDAR.....DAVRKAAAGTTTAPASASA 126

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlpl
-O=/cgn2 1/USPTO spool p/US10005429/runat 04052004 121649 15445/app query.fasta_1.782
-DB=SST -QFMT=fastap -SUPFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human0.cdi -LIST=45
-DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10005429 @CGN 1 1 5436 runat 04052004 121649 15445 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOF=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hcc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hcc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	623.5	95.6	496	14	CF007924 QB16a01.x
2	623.5	95.6	503	14	CF019426 QB16a01.x
3	623.5	95.6	562	14	CF005608 QB113B03.
4	621	95.2	427	14	CF647253 3530_1_41
5	618.5	94.9	568	14	CF020146 QB2B06.x
6	615.5	94.4	503	14	CF019553 QB1h06.x
7	615.5	94.4	504	14	CF019475 QB1h06.x
8	610	93.6	388	12	EG837010 Zm08_10f0
9	605.5	92.9	442	14	CD974597 QAE48B02.
10	600.5	92.1	411	14	CD976888 QAF23B09.
11	600.5	92.1	430	14	CD972346 QAE20B03.
12	600.5	92.1	480	14	CD978907 QAF6f04.Y
13	580	89.0	456	12	BG837151 Zm08_06b0
14	574.5	88.1	426	14	CF008093 QB17B05.x
15	568.5	87.2	573	14	CF006552 QB120C10.
16	561.5	86.1	400	14	CD974844 QAE50C02.
17	496.5	76.2	359	14	CF008092 QB17B05.P
18	480.5	73.7	681	28	BZ794456 PUGEZ32TB
19	466.5	71.5	859	29	CG158805 PUFVJ10TB
20	466.5	71.5	953	29	CG323449 QGWFP30TV
21	465.5	71.4	873	29	CG323435 QGWFP30TV
22	456	69.9	370	14	CF006994 QB124F08.
23	433.5	66.5	519	14	CA273890 SCRLSD101
24	399	61.2	658	14	CA277200 SCRLSD201
25	399	61.2	1056	14	CA275558 SCRLSD103
26	369	56.6	528	14	CB214678 OML04958
27	369	56.6	538	14	CB211098 OML01378
28	369	56.6	639	14	CB213067 OML03347
29	364.5	55.9	316	14	CD949589 SAE_90 Ge
30	361	55.4	467	9	AU057218 AU057218
31	361	55.4	493	14	CF320119 HD--10-O0
32	361	55.4	495	14	CF299663 7LEAF--03
33	361	55.4	515	14	CF314470 HD--03-A0
34	361	55.4	527	9	AU063587 AU063587
35	361	55.4	549	13	BQ283661 WHE30394.H
36	361	55.4	551	14	CF330192 NACL--05-
37	361	55.4	553	14	CF315555 HD--04-I0
38	361	55.4	581	14	CF304186 ABE1--04-
39	361	55.4	611	14	CF307434 HDA1--06-
40	361	55.4	612	14	CF319360 HD--09-N0
41	361	55.4	613	14	CF305242 CLD1--01-
42	361	55.4	663	13	BQ283448 WHE30391.C
43	361	55.4	665	14	CF321946 HD--13-F2
44	361	55.4	776	14	CA758876 BRU500010
45	360	55.2	498	14	CF338577 RCU1--02-

ALIGNMENTS

RESULT 1
CF007924 496 bp mRNA linear EST 16-JUL-2003
LOCUS QB16a01.xg QB1 Zea mays cDNA clone QB16a01, mRNA sequence.
DEFINITION CF007924
ACCESSION CF007924
VERSION CF007924.1 GI:32868242
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 496)

AUTHORS Genoplante.
 TITLE Genoplante, a major partnership french program in plant genomics
 JOURNAL Unpublished (2003)
 COMMENT Contact: Genoplante
 Genoplante
 93, rue Henri Rochefort 91025 EVRY CEDEX France
 Tel: 33 1 69 47 54 00
 Fax: 33 1 69 47 54 10
 This sequence has been generated in the framework of the french
 plant genomics programme 'Genoplante' (http://www.genoplante.com
 and http://genoplante-info.infobiogen.fr).

FEATURES
 source
 1. .496
 /organism="Zea mays"
 /mol_type="mRNA"
 /cultivar="P2"
 /db_xref="taxon:4577"
 /clone="QB16a01"
 /tissue_type="pedicel"
 /clone_lib="QBI"

ORIGIN
 Alignment Scores:
 Pred. No.: 1.75e-69 Length: 496
 Score: 623.50 Matches: 126
 Percent Similarity: 98.44% Conservative: 0
 Best Local Similarity: 98.44% Mismatches: 0
 Query Match: 95.63% Indels: 2
 DB: 14 Gaps: 1

US-10-005-429-14 (1-126) x CF007324 (1-496)

QY 1 MetAlaAGluGluGlyAlaValIleAlaCysHisThrLysAspGluPheAlaArg 20
 DB 65 ATGGCGCGGAGGAGGCGCGGATCGCGTGCACACCAAGAGCGAGTTTCAGCGCCGC 124
 QY 21 MetAlaValAlaLysGluGlnGlyLysLeuValValIleAsp----PheMetAlaProTr 39
 DB 125 ATGGCAAGGCCAAGGAGGAGGCGAGCTGGTGTCTATCGACTTCGTTTCATGGCCCCCTG 184
 QY 39 pCysSerGlyCysGlnMetMetAlaProValTyrAlaAspCysAlaSerLysTyrProSe 59
 DB 185 GTGCAGTGGTGTCCAGATGATGCCCCCGGTGTACGGGAGCTGCGCAGCAAGTACCTTTC 244
 QY 59 rAlaValPheLeuGluValAspValAspGluLeuGluValAlaLysIleTyrGlyVa 79
 DB 245 CGCGGTCTTCCTCGAGGTGCAGTGCAGCAACTGCTGGAAGTGCAGGAGATCTACGGCGT 304
 QY 79 lHisValMetProThrPheCysPheIleATGAsnGlyGluThrLeuGluSerPheAlaTh 99
 DB 305 CCATGTGATGCCGACCTTCTGCTTCATCAGGAACGGCGAGAGCTTCGAGAGCTTTGCTAC 364
 QY 99 rValAspGluAspGluLeuArgAspAlaValArgLysTyrAlaAlaGlyThrThrTh 119
 DB 365 CGTCGACGAGGAGAGCTCCGGAGCGCGTCAGGAAGTACGGCGCTGGCACTACGAC 424
 QY 119 rAlaProAlaSerAlaSerAla 126
 DB 425 GGCTCTGCTCGCGGTCGCC 446

RESULT 2
 CF019426
 LOCUS CF019426 503 bp mRNA linear EST 17-JUL-2003
 DEFINITION QBN19c09.xg QBN Zea mays cDNA clone QBN19c09, mRNA sequence.
 ACCESSION CF019426
 VERSION CF019426.1 GI:32914614
 KEYWORDS EST.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 Clade; Panicoideae; Andropogoneae; Zea.
 REFERENCE 1 (bases 1 to 503)

AUTHORS Genoplante.
 TITLE Genoplante, a major partnership french program in plant genomics
 JOURNAL Unpublished (2003)
 COMMENT Contact: Genoplante
 Genoplante
 93, rue Henri Rochefort 91025 EVRY CEDEX France
 Tel: 33 1 69 47 54 00
 Fax: 33 1 69 47 54 10
 This sequence has been generated in the framework of the french
 plant genomics programme 'Genoplante' (http://www.genoplante.com
 and http://genoplante-info.infobiogen.fr).

FEATURES
 source
 1. .503
 /organism="Zea mays"
 /mol_type="mRNA"
 /cultivar="P2"
 /db_xref="taxon:4577"
 /clone="QBN19c09"
 /tissue_type="pedicel, whole kernel"
 /clone_lib="QBN"

ORIGIN
 Alignment Scores:
 Pred. No.: 1.79e-69 Length: 503
 Score: 623.50 Matches: 126
 Percent Similarity: 98.44% Conservative: 0
 Best Local Similarity: 98.44% Mismatches: 0
 Query Match: 95.63% Indels: 2
 DB: 14 Gaps: 1

US-10-005-429-14 (1-126) x CF019426 (1-503)

QY 1 MetAlaAGluGluGlyAlaValIleAlaCysHisThrLysAspGluPheAlaArg 20
 DB 65 ATGGCGCGGAGGAGGCGCGGATCGCGTGCACACCAAGAGCGAGTTTCAGCGCCGC 124
 QY 21 MetAlaValAlaLysGluGlnGlyLysLeuValValIleAsp----PheMetAlaProTr 39
 DB 125 ATGGCAAGGCCAAGGAGGAGGCGAGCTGGTGTCTATCGACTTCGTTTCATGGCCCCCTG 184
 QY 39 pCysSerGlyCysGlnMetMetAlaProValTyrAlaAspCysAlaSerLysTyrProSe 59
 DB 185 GTGCAGTGGTGTCCAGATGATGCCCCCGGTGTACGGGAGCTGCGCAGCAAGTACCTTTC 244
 QY 59 rAlaValPheLeuGluValAspValAspGluLeuGluValAlaLysIleTyrGlyVa 79
 DB 245 CGCGGTCTTCCTCGAGGTGCAGTGCAGCAACTGCTGGAAGTGCAGGAGATCTACGGCGT 304
 QY 79 lHisValMetProThrPheCysPheIleATGAsnGlyGluThrLeuGluSerPheAlaTh 99
 DB 305 CCATGTGATGCCGACCTTCTGCTTCATCAGGAACGGCGAGAGCTTCGAGAGCTTTGCTAC 364
 QY 99 rValAspGluAspGluLeuArgAspAlaValArgLysTyrAlaAlaGlyThrThrTh 119
 DB 365 CGTCGACGAGGAGAGCTCCGGAGCGCGTCAGGAAGTACGGCGCTGGCACTACGAC 424
 QY 119 rAlaProAlaSerAlaSerAla 126
 DB 425 GGCTCTGCTCGCGGTCGCC 446

RESULT 3
 CF005608
 LOCUS CF005608 562 bp mRNA linear EST 16-JUL-2003
 DEFINITION QBI13b03.xg QBI Zea mays cDNA clone QBI13b03, mRNA sequence.
 ACCESSION CF005608
 VERSION CF005608.1 GI:32865926
 KEYWORDS EST.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 Clade; Panicoideae; Andropogoneae; Zea.
 REFERENCE 1 (bases 1 to 562)

AUTHORS Genoplante.
TITLE Genoplante, a major partnership french program in plant genomics
JOURNAL Unpublished (2003)
COMMENT Contact: genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (<http://www.genoplante.com>
and <http://genoplante-info.infobiogen.fr>).

```

FEATURES
source
1. 562
Location/Qualifiers
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="P2"
/db_xref="taxon:4577"
/clone="QB13b03"
/tissue_type="pedicel"
/clone_lib="OBI"

```

```

ORIGIN
Alignment Scores:
  Pred. No.:      2,11e-69
  Score:          623.50
  Percent Similarity: 98.44%
  Best Local Similarity: 98.44%
  Query Match:    95.63%
  DB:             14
                Length: 562
                Matches: 126
                Conservative: 0
                Mismatches: 0
                Indels: 2
                Gaps: 1
US-10-005-429-14 (1-126) x CF005608 (1-562)

```

Qy 1 MetAlaAlaGluGluGlyAlaValIleAlaCysHisThrIysAspGluPheAspAlaArg 20
Db 65 ATGCGCGCGGAGAGGGTCCGTGATCGCTGCCACACCAAGACAGAGTTTCAGACGCCGC 124

21 MetAlaLysAlaLysGluGlnGlyLysLeuValValIleasp----PheMetAlaProTr 39
125 ATGGCCAGAGCCACAGGACAGGCGAAGCTGGTGGTCTGACTTGGTTCATGCCCCCGG 184

39 pCysSerGlyCysGlnMetMetAlaProValIyrAlaAspCysAlaSerIysIyrProSe 59
185 GTGCAGTGGGTGCCAGATGATGGCCCGCGTGTACCGGACTGGCCAGCAAGTACCGCTTC 244

59 rAlaValPheIeuGluValAspValAspGluLeuLeuGluValAlaLysIleTyrGlyVa 79
245 CCGCGTCCTCTCGAGSTCGACSTCGACGACTCTCTGCAAGTCGCGAAGATCTACGGST 304

79 LHisValMetProThrPheCysPheIleArgAsnGlyGluThrLeuGluSerPheAlath 99
305 CCATGTGATGCCAGCATCTTGTTTCATCAGAAACGGCAGACGCTCCAGAGCTTCTCAC 364

Qy	99	rValAspGluAspGluLeuAspAlaValArgCysTyrAlaAlaGlyThrThr	119
Db	365	CETCCACAGGAGACAGTCCCGGACCGCGTCAGAGTACGCGCGCTGGCATACAC	424

	CGTCTGACGGAGCAGCAATGAGGGG
Qy	119 rAlaProLaserAlaSerAla 126
	GCCTCTGTCCTGGGTCCGCC
Dd	425 GCCTCTGTCCTGGGTCCGCC 446

LOCUS	CF647253	427 bp	mrna	linear	EST 02-OCT-2000
RESULT 4	CF647253				
LOCUS	CF647253	427 bp	mrna	linear	EST 02-OCT-2000

3530.1_41.1 D03.x 1 3530 - Full length cDNA library created by
Invitrogen from multiple tissues Zea mays cDNA, mRNA sequence.
CF647253
ACCESSION
VERSION
GI:37419153

RECORD	DATE	KEYWORDS	SOURCE	ORGANISM
1000000000	1970-12-15	EST.	Zea mays	
1000000000	1970-12-15		Zea mays	
1000000000	1970-12-15			Streptophyta; Embryophyta Tracheophyta; Eukaryota: Viridiplantae;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

REFERENCE AUTHORS TITLE	JOURNAL	COMMENT
1 (bases 1 to 427) Walbot,V. Maize ESTs from var University	Unpublished (1999)	Contact: Walbot V

Department of Biological Sciences
Stanford University
895 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 3530 1 411 row: D column: 03.

```

FEATURES
Location/Qualifiers
1. .427
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="B73"
/db_xref="taxon:4577"
/tissue_type="multiple"
/dev_stage="varies by tissue"
/lab_host="DH10B"

```

/clone_lib=r3530 - Full length cDNA library created by nitrogen from multiple tissues"
/notes=Organ: silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo; Vector: pCMV-SPORT 6.1; Site 1: EcoRV; Site 2: NotI; Maize Gene Discovery Project contracted with Invitrogen to produce a normalized, full length library in a pSPORT vector. This is a Gateway compatible vector, permitting clone movement to new vector backbones for expression in diverse host cells using recombination rather than restriction enzymes. Details of the vector and sequencing primers are available at ZmDB in the EST library description tables. poly(A)+ mRNA was prepared by Invitrogen, and equimolar amounts of RNA from each of the 12 tissue samples were mixed together for selection of mRNA with a 5' cap. After synthesis of cDNA, a normalization step was conducted against the mixture of RNA sources. This step effected a 20X to 80X reduction in common transcript types. Tissues prepared: 1. just emerging silks; 2. inner husks from ears of sample #1; 3. 20 day aleurone; 4. immature tassels, stages from 1.2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from 15 day old seedlings; all leaves with an expanded or partially expanded sheath were removed; 8. mature leaf tissue; 9. 0.5 cm long root tips from 15 day old seedlings; 10. 10 day whole seed; 11. 12 day endosperm and embryo; 12. 17 day endosperm and embryo. All of the sequenced clones in project 3530 will be archived at the University of Arizona along with the unigene clones from the Maize Gene Discovery EST sequencing projects. Clones can be ordered through the ZmDB web site or directly from the University of Arizona (<http://www.genome.arizona.edu/orders/>). High density filters containing over 18,000 clones can also be ordered from the University of Arizona."

ORIGIN

Alignment Scores:	2, 93e-69	Length:	427
Pred. No.:	21.00	Matches:	119
Score:	62.00	Conservative:	0
Percent Similarity:	98.33%	Mismatches:	2
Best Local Similarity:	98.33%	Indels:	0
Query Match:	95.25%	Gaps:	0
DB:	14		

US-10-005-429-14 (1-126) x CF647253 (1-427)

Qy 1 MetAlaAlaGluGluGlyAlaValIleAlaCysHisThrLysAspGluPheAspAlaArg 20

Db	54	ATGGCGCGGAGAGCGGTGCGTGCATCGGTGCACACCAAGGACGAGTTGACGCGCGC	123
Ov	21	MetA[alv]sAlatvsgGluGlnGlvLvsLeuValValIleAspPheMetAlaProTrpCys	40

100

```

Db      124 ATGCCAAGCCAGGAGGAGGCAAGCTGTGTATCATGCTTCATGGCCCCCTGGTGC 183
Qy      41 SerGlyCysGlnMetMetAlaProValTyrAlaAspCysAlaSerLysTyrProSerAla 60
Db      184 AGTGGGTGCCAGATGATGGCCCCCGTGTACGCGACTGCGCCAGCAAGTACCCCTTCGGCG 243
Qy      61 ValPheLeuGluValAspValAspGluLeuGluValAlaLysTyrGlyValHis 80
Db      244 GTCCTCTTCGAGGTGCGACGTGCGACCACTGCTGGAAGTCCGGAAGTCTACGGCGTCCAT 303
Qy      81 ValMetProThrPheCysPheIleArgAsnGlyGluThrLeuGluSerPheAlaThrVal 100
Db      304 GTGATGCGGACCTTCTGCTTCATCAGGAACGGGAGACGCTCGAGAGCTTGTACCGTC 363
Qy      101 AspGluAspGluLeuArgAspAlaValArgLysTyrAlaAlaGlyThrThrAla 120
Db      364 GACGAGAGAGAGCTCCGGGACGCGCTGAGGANTATCCCCCGCTGGCACTACGACGCT 423
Qy      121 Pro 121
Db      424 CCT 426

RESULT 5
LOCUS   CF020146 568 bp mRNA linear EST 17-JUL-2003
DEFINITION QN2B06.XG QBN Zea mays cDNA clone QN2B06, mRNA sequence.
ACCESSION CF020146
VERSION   CF020146.1 GI:32915334
KEYWORDS EST.
SOURCE   Zea mays
ORGANISM Zea mays
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
TITLE clade; Panicoidae; Andropogoneae; Zea.
JOURNAL 1 (bases 1 to 568)
COMMENT Genopiante.
        Genopiante, a major partnership french program in plant genomics
        Unpublished (2003)
        Contact: Genopiante
        Genopiante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genopiante' (http://www.genopiante.com)
and http://genopiante-info.infobiogen.fr.

FEATURES             source
    source
    1..568
        /organism="Zea mays"
        /mol_type="mRNA"
        /cultivar="F2"
        /db_xref="taxon:4577"
        /clone="QN2B06"
        /tissue_type="pedicel, whole kernel"
        /clone_lib="QBN"

ORIGIN
Alignment Scores:
Pred. No.: 9.37e-69 Length: 568
Score: 618.50 Matches: 125
Percent Similarity: 98.44% Conservative: 1
Best Local Similarity: 97.66% Mismatches: 0
Query Match: 94.86% Indels: 2
DB: 14 Gaps: 1

US-10-005-429-14 (1-126) x CF020146 (1-568)

Qy      1 MetAlaGluGluGlyAlaValIleAlaCysHisThrLysAspGluPheAspAlaArg 20
Db      65 ATGGCGCCGAGGAGGCTCGGTGATCGGTGCCACACCAAGGACGAGTTCGACGCCCGC 124
Qy      21 MetAlaLysAlaLysGluGlnGlyLysLeuValValIleAsp----PheMetAlaProTr 39

```

```

Db      125 ATGGCCAGGCGCAGGAGGAGGCAAGCTGTGTATCATGCTTCATGGCCCCCTG 184
Qy      39 pCysSerGlyCysGlnMetMetAlaProValTyrAlaAspCysAlaSerLysTyrProSe 59
Db      185 GTGCAGTGGGTGCCAGATGATGGCCCCCGTGTACGCGACTGCGCCAGCAAGTACCCCTTC 244
Qy      59 rAlaValPheLeuGluValAspValAspGluLeuGluValAlaLysTyrGlyVal 79
Db      245 CGCGGTCTTCTCGAGGTGCGACGTGCGACCACTGCTGGAAGTCCGGAAGTCTACGGCGT 304
Qy      79 lHisValMetProThrPheCysPheIleArgAsnGlyGluThrLeuGluSerPheAlaTh 99
Db      305 CCATGTGATGCGGACCTTCTGCTTCATCAGGAACGGGAGACGCTCGAGAGCTTGTGTAC 364
Qy      99 rValAspGluAspGluLeuArgAspAlaValArgLysTyrAlaAlaGlyThrThrTh 119
Db      365 CGTCAAGAGAGAGCGAGTCCGGGAGCGCGTCAAGAGTACGCGCGCTGGCACTACGAC 424
Qy      119 rAlaProAlaSerAlaSerAla 126
Db      425 GGCTCTGCTCGCTCGCGTCCGCC 446

RESULT 6
LOCUS   CF019553 503 bp mRNA linear EST 17-JUL-2003
DEFINITION QBNih06.XG QBN Zea mays cDNA clone QBNih06, mRNA sequence.
ACCESSION CF019553
VERSION   CF019553.1 GI:32914741
KEYWORDS EST.
SOURCE   Zea mays
ORGANISM Zea mays
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
TITLE clade; Panicoidae; Andropogoneae; Zea.
JOURNAL 1 (bases 1 to 503)
COMMENT Genopiante.
        Genopiante, a major partnership french program in plant genomics
        Unpublished (2003)
        Contact: Genopiante
        Genopiante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genopiante' (http://www.genopiante.com)
and http://genopiante-info.infobiogen.fr.

FEATURES             source
    source
    1..503
        /organism="Zea mays"
        /mol_type="mRNA"
        /cultivar="F2"
        /db_xref="taxon:4577"
        /clone="QBNih06"
        /tissue_type="pedicel, whole kernel"
        /clone_lib="QBN"

ORIGIN
Alignment Scores:
Pred. No.: 1.9e-68 Length: 503
Score: 615.50 Matches: 124
Percent Similarity: 97.66% Conservative: 1
Best Local Similarity: 96.88% Mismatches: 1
Query Match: 94.40% Indels: 2
DB: 14 Gaps: 1

US-10-005-429-14 (1-126) x CF019553 (1-503)

Qy      1 MetAlaGluGluGlyAlaValIleAlaCysHisThrLysAspGluPheAspAlaArg 20
Db      65 ATGGCGCCGAGGAGGCTCGGTGATCGGTGCCACACCAAGGACGAGTTCGACGCCCGC 124
Qy      21 MetAlaLysAlaLysGluGlnGlyLysLeuValValIleAsp----PheMetAlaProTr 39

```

```

Db      125 ATGCCAAGCCAGGAGGAGGCAAGCTGTGTTTCATCGACTTCGTTTCATGGCCCCCTG 184
Qy      39 pCysSerGlyCysGlnMetMetAlaProValTyrAlaAspCysAlaSerLysTyrProSe 59
Db      185 GTGCAGTGGGTGCCAGATGATGGCCCCGGGTGTACGGGACTTGGCCAGCAAGTACCCCTTC 244
Qy      59 rAlaValPheLeuGluValAspValAspGluLeuGluValAlaAlaLysIleTyrGlyVa 79
Db      245 CGCGGTCTTCTCGAGGTGCGACGTGCGAGCACTGCTGGAAGTCGCGAAGATCTACGGCGT 304
Qy      79 LHisValMetProThrPheCysPheIleArgAsnGlyGluThrLeuGluSerPheAlaTh 99
Db      305 CCATGTGATGCGGACCTTCTCTTCATCATCAGAAACGGGAGACGCTCGAGAGCTTTGTCTAC 364
Qy      99 rValAspGluAspGluLeuArgAspAlaValAlaLysTyrAlaAlaGlyThrThrTh 119
Db      365 CGTCGACGAGGACGAGTCTCCGGACGCGCTCAGGAGTACCGCCCGCTGGCACTACGAC 424
Qy      119 rAlaProAlaSerAlaSerAla 126
Db      425 GGCTCCTCGCTCGGCGTCCGCC 446

```

```

RESULT 7
CF019475 QBN19405.xg QBN Zea mays cDNA clone QBN19405, mRNA sequence. EST 17-JUL-2003
LOCUS QBN19405
DEFINITION QBN19405
ACCESSION CF019475
VERSION QBN19475.1 GI:32914663
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 504)
AUTHORS Genoplante.
TITLE Genoplante, a major partnership french program in plant genomics
JOURNAL Unpublished (2003)
COMMENT Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com)
and http://genoplante-info.infobiogen.fr.
Location/Qualifiers
FEATURES
source
1..504
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="P2"
/db_xref="taxon:4577"
/clone="QBN19405"
/tissue type="pedicel, whole kernel"
/clone_lib="QBN"

```

```

ORIGIN
Alignment Scores:
Pred. No.: 1.9e-68 Length: 504
Score: 615.50 Matches: 124
Percent Similarity: 97.66% Conservative: 1
Best Local Similarity: 96.88% Mismatches: 2
Query Match: 94.40% Indels: 2
DB: 14 Gaps: 1

```

US-10-005-429-14 (1-126) x CF019475 (1-504)

```

Qy      1 MetAlaAlaGluGluGluValAlaValIleAlaCysHisThrLysAspGluPheAspAlaArg 20
Db      64 ATGGCGGCGGAGGAGGCTGGTGTATCGGTGTCACACACCAAGGAGGAGTTCGACGCCCGC 123
Qy      21 MetAlaLysAlaLysGluGlnGlyLysLeuValIleAsp----PheMetAlaProThr 39

```

```

Db      124 ATGCCAAGCCAGGAGGAGGCAAGCTGTGTTTCATCGACTTCGTTTCATGGCCCCCTG 183
Qy      39 pCysSerGlyCysGlnMetMetAlaProValTyrAlaAspCysAlaSerLysTyrProSe 59
Db      184 GTGCAGTGGGTGCCAGATGATGGCCCCGGGTGTACGGGACTTGGCCAGCAAGTACCCCTTC 243
Qy      59 rAlaValPheLeuGluValAspValAspGluLeuGluValAlaAlaLysIleTyrGlyVa 79
Db      244 CGCGGTCTTCTCGAGGTGCGACGTGCGAGCACTGCTGGAAGTCGCGAAGATCTACGGCGT 303
Qy      79 LHisValMetProThrPheCysPheIleArgAsnGlyGluThrLeuGluSerPheAlaTh 99
Db      304 CCATGTGATGCGGACCTTCTCTTCATCATCAGAAACGGGAGACGCTCGAGAGCTTTGTCTAC 363
Qy      99 rValAspGluAspGluLeuArgAspAlaValAlaLysTyrAlaAlaGlyThrThrTh 119
Db      364 CGTCGACGAGGACGAGTCTCCGGACGCGCTCAGGAGTACCGCCCGCTGGCACTACGAC 423
Qy      119 rAlaProAlaSerAlaSerAla 126
Db      424 GGCTCCTCGCTCGGCGTCCGCC 445

```

```

RESULT 8
BG837010/c BG837010 388 bp mRNA linear EST 25-MAY-2001
LOCUS Zm08_AAFc_EC0RC_Fusarium graminearum_inoculated_corn_ear_Zea mays
DEFINITION Zm08_AAFc_EC0RC_Fusarium graminearum_inoculated_corn_ear_Zea mays
cDNA clone Zm08_10f04, mRNA sequence.
ACCESSION BG837010
VERSION BG837010.1 GI:14203333
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 388)
AUTHORS Harris,L.J., Balcerzak,M., Allard,S., Saparno,A., Couroux,P., De
Moors,A., Hattori,J.I., Ouellet,T., Robert,L.S., Singh,J.A.,
Spratt,D. and Tinker,N.A.
TITLE Expressed Sequence Tags from Developing Maize Kernels Six Days
after Silk Channel Inoculation with Fusarium graminearum
JOURNAL Unpublished (2001)
COMMENT Contact: Harris, Linda J.
Eastern Cereal and Oilseed Research Centre
Agriculture and Agri-food Canada
Bldg. 21, Central Experimental Farm, Ottawa, Ontario, KIA 0C6,
CANADA
Tel: (613) 759-1314
Fax: (613) 759-6566
Email: harris@em.agr.ca.
Location/Qualifiers
FEATURES
source
1..388
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="CO430"
/db_xref="taxon:4577"
/clone="Zm08_10f04"
/tissue type="Developing kernels (sibcrossed)"
/dev_stage="10-11 days post-silk emergence"
/clone_lib="Zm08_AAFc_EC0RC_Fusarium graminearum_inoculate
d_corn_ear"
/notes="vector: Bluescript SK+/XhoI-EC0RI; Site_1: EC0RI;
Site_2: XhoI; Field-grown maize ears were silk
channel-inoculated in the morning (~10 am) with 1 ml of a
Fusarium graminearum macroconidial suspension (500,000
spores/ml) and whole ears were collected and immediately
frozen in liquid nitrogen 6 days later."

```

ORIGIN

```

Alignment Scores:
Pred. No.: 6.56e-68 Length: 388

```

Score:	610.00	Matches:	117
Percent Similarity:	99.16%	Conservative:	1
Best Local Similarity:	98.32%	Mismatches:	1
Query Match:	93.56%	Indels:	0
DB:	12	Gaps:	0
US-10-005-429-14 (1-126) x BG837010 (1-388)			
QY	8	ValIleAlaCysHisThrLysAspGluPheAspAlaArgMetAlaLysAlaLysGluGln	27
DB	387	GTGATCGCGTCATACCAAGACGAGTTCCGACGCCCGCATGCGCCCAAGGCCAAGGAGGAG	328
QY	28	GlyLysLeuValValIleAspPheMetAlaProTyrCysSerGlyCysGlnMetMetAla	47
DB	327	GCAAGCTGGTGCATCGACTTCATGGCCCTCGTGCAGTGGTGCAGATGATGGCC	268
QY	48	ProValTyrAlaAspCysAlaSerLysTyrProSerAlaValPheLeuGluValAspVal	67
DB	267	CCGGTGTACCGGACTGCGCCAGCAAGTACCCCTTCGCGGCTTCCTCGAGTTCGAGCTC	208
QY	68	AspGluLeuGluValAlaLysIleTyrGlyValHisValMetProThrPheCysPhe	87
DB	207	GACGAACCTGCGAAGTCGCGAAGATCTACGGCGTCCATGTGATGCGGACCTTCGCTTC	148
QY	88	IleArgAsnGlyClnThrLeuGluSerPheAlaThrValAspGluAspGluLeuArgAsp	107
DB	147	ATCAGGAACGGGAGACGCTCGAGAGCTTTGCTACCGTCCGACGAGGACGACCTCCGGGAC	88
QY	108	AlaValArgLysTyrAlaAlaGlyThrThrAlaProAlaSerAlaSerAla	126
DB	87	GCGGTCAGGAAGTACCGCGCGCTGGCACTACGACGGCTCCTGGCGCTCGCGTCCGCGC	31
RESULT 9			
CD974597/c	442 bp	mRNA	linear
LOCUS	QAE48b02.yg	QAE	48b02, mRNA sequence.
DEFINITION	QAE48b02.yg	QAE	48b02, mRNA sequence.
ACCESSION	CD974597		
VERSION	CD974597.1	GI:32834913	
KEYWORDS	EST.		
SOURCE	Zea mays		
ORGANISM	Zea mays		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoidae; Andropogoneae; Zea.		
AUTHORS	1 (bases 1 to 442)		
TITLE	Genopiante.		
JOURNAL	Genopiante, a major partnership french program in plant genomics		
COMMENT	Unpublished (2003)		
CONTACT	Contact: Genopiante		
Genopiante	93, rue Henri Rochefort 91025 EVRY CEDEX France		
Tel:	33 1 69 47 54 00		
Fax:	33 1 69 47 54 10		
This sequence has been generated in the framework of the french plant genomics programme 'Genopiante' (http://www.genopiante.com and http://genopiante-info.infobiogen.fr).			
FEATURES	Location/Qualifiers		
source	1..442		
	/organism="Zea mays"		
	/mol_type="mRNA"		
	/cultivar="P2"		
	/db_xref="taxon:4577"		
	/clone="QAE48b02"		
	/tissue_type="pericarp"		
	/clone_lib="QAE"		
ORIGIN			
Alignment Scores:			
Pred. No.:	3.01e-67	Length:	442
Score:	605.50	Matches:	122
Percent Similarity:	97.66%	Conservative:	3
Best Local Similarity:	95.31%	Mismatches:	1
Query Match:	92.87%	Indels:	2

DB:	14	Gaps:	1
US-10-005-429-14 (1-126) x CD974597 (1-442)			
QY	1	MetAlaAlaGluGlyAlaValIleAlaCysHisThrLysAspGluPheAspAlaArg	20
DB	435	GTCCGGCCCAAGGAGGTCCTCGATCCGTCACACCAAGGACGAGTTCACGCCCGC	376
QY	21	MetAlaLysAlaLysGluGlnGlyLysLeuValValIleAsp----PheMetAlaProTyr	39
DB	375	ATGGCCCAAGGCCAAGGACGAGCTGGTGGTGCATCGACTTCGTTTCATGGCCCGCTG	316
QY	39	PcySerGlyCysGlnMetMetAlaProValTyrAlaAspCysAlaSerLysTyrProSe	59
DB	315	GTGCAGTGGGTGCAGATGATGCGCCCGTGTACGGGACTGCGCCCAAGGACGAGTTC	256
QY	59	rAlaValPheLeuGluValAspValAspGluLeuGluValAlaLysIleTyrGlyVa	79
DB	255	CGCGTCTCTTCGAGGTGCGAGTCTGCAAGTCTGCAAGTCTGCAAGTCTACGGCGT	196
QY	79	IHisValMetProThrPheCysPheIleArgAsnGlyClnThrLeuGluSerPheAlaTh	99
DB	195	CCATGTGATGCGGACCTTTTGTCTTCATCAGAAACGGCGAGACGCTCGAGAGCTTTGCTAC	136
QY	99	rValAspGluAspGluLeuArgAspAlaValArgLysTyrAlaAlaGlyThrThrTh	119
DB	135	CGTCGACGAGGACGAGCTCCGGGACGCGCTCAGGAGTACGCGCGCTGGCAGCTACGAC	76
QY	119	rAlaProAlaSerAlaSerAla	126
DB	75	GCGTCTCGCTCGGCGTCCGCGC	54
RESULT 10			
CD976888	411 bp	mRNA	linear
LOCUS	QAF23b09.yg	QAF	23b09, mRNA sequence.
DEFINITION	QAF23b09.yg	QAF	23b09, mRNA sequence.
ACCESSION	CD976888		
VERSION	CD976888.1	GI:32837210	
KEYWORDS	EST.		
SOURCE	Zea mays		
ORGANISM	Zea mays		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoidae; Andropogoneae; Zea.		
AUTHORS	1 (bases 1 to 411)		
TITLE	Genopiante.		
JOURNAL	Genopiante, a major partnership french program in plant genomics		
COMMENT	Unpublished (2003)		
CONTACT	Contact: Genopiante		
Genopiante	93, rue Henri Rochefort 91025 EVRY CEDEX France		
Tel:	33 1 69 47 54 00		
Fax:	33 1 69 47 54 10		
This sequence has been generated in the framework of the french plant genomics programme 'Genopiante' (http://www.genopiante.com and http://genopiante-info.infobiogen.fr).			
FEATURES	Location/Qualifiers		
source	1..411		
	/organism="Zea mays"		
	/mol_type="mRNA"		
	/cultivar="P2"		
	/db_xref="taxon:4577"		
	/clone="QAF23b09"		
	/tissue_type="pericarp"		
	/clone_lib="QAF"		
ORIGIN			
Alignment Scores:			
Pred. No.:	1.18e-66	Length:	411
Score:	600.50	Matches:	121
Percent Similarity:	98.37%	Conservative:	0
Best Local Similarity:	98.37%	Mismatches:	0
Query Match:	92.10%	Indels:	2

DB:	14	Gaps:	1
US-10-005-429-14 (1-126) x CD972346 (1-430)			
QY	6	GlyAlaValIleAlaCysHisThrLysAspGluPheAspAlaArgMetAlaLysAlaLys	25
Db	3	GGTGGCGTATCGGTGCCACCAAGGACGAGTTTCGACCGCCCGATGGCCAAAGGCAAG	62
QY	26	GluGlnGlyLysLeuValValIleAsp----PheMetAlaProTTPCysSerGlyCysG	44
Db	63	GAGCAGGGCAAGCTGGTGGTCATCGACTTCGTTTCATGGCCCCCTGGTGGTGGTGGCA	122
QY	44	nMetMetAlaProValTyAlaAspCysAlaSerLysTyProSerAlaValPheLeuG	64
Db	123	GATGATGGCCCCGCTGATCGCGGACTCGCCAGCAAGTACCTTCGCGGTTCCTCGA	182
QY	64	uValAspValAspGluLeuLeuGluValAlaLysIleTyGlyValHisValMetProTh	84
Db	183	GGTCGAGCTCGACCAACTGCTGGAAGTCGGAAGATCTACGGGCTCATGTGATCGGAC	242
QY	84	rPheCysPheIleArgSerGlyGluThrLeuGluSerPheAlaThrValAspGluAspG	104
Db	243	CTTCTGCTTCATCAGGAACGGCGAGACGCTCGAGAGCTTTGCTACCGTCCGAGGACGA	302
QY	104	uLeuArgAspAlaValArgLysTyAlaAlaAlaGlyThrThrAlaProAlaSerAl	124
Db	303	GCTCCGGGACCGCTCAGGAAGTACGGCGGCTGGCACTACGACGGCTCTGCTCGGC	362
QY	124	aSerAla 126	
Db	363	GTCCGCC 369	
RESULT 12			
CD978907			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
COMMENT			
FEATURES			
source			
ORIGIN			
Alignment Scores:			
Pred. No.:			
Score:			
Percent Similarity:			
Best Local Similarity:			
Query Match:			

US-10-005-429-14 (1-126) x CD972346 (1-430)	1
GlyAlaValIleAlaCysHisThrLysAspGluPheAspAlaArgMetAlaLysAlaLys	25
GGTGGCGTATCGGTGCCACCAAGGACGAGTTTCGACCGCCCGATGGCCAAAGGCAAG	62
GluGlnGlyLysLeuValValIleAsp----PheMetAlaProTTPCysSerGlyCysG	44
GAGCAGGGCAAGCTGGTGGTCATCGACTTCGTTTCATGGCCCCCTGGTGGTGGTGGCA	122
nMetMetAlaProValTyAlaAspCysAlaSerLysTyProSerAlaValPheLeuG	64
GATGATGGCCCCGCTGATCGCGGACTCGCCAGCAAGTACCTTCGCGGTTCCTCGA	182
uValAspValAspGluLeuLeuGluValAlaLysIleTyGlyValHisValMetProTh	84
GGTCGAGCTCGACCAACTGCTGGAAGTCGGAAGATCTACGGGCTCATGTGATCGGAC	242
rPheCysPheIleArgSerGlyGluThrLeuGluSerPheAlaThrValAspGluAspG	104
CTTCTGCTTCATCAGGAACGGCGAGACGCTCGAGAGCTTTGCTACCGTCCGAGGACGA	302
uLeuArgAspAlaValArgLysTyAlaAlaAlaGlyThrThrAlaProAlaSerAl	124
GCTCCGGGACCGCTCAGGAAGTACGGCGGCTGGCACTACGACGGCTCTGCTCGGC	362
aSerAla 126	
GTCCGCC 369	
CD972346	430 bp mRNA linear EST 16-JUL-2003
QAE20603.yg QAE Zea mays cDNA clone QAE20603, mRNA sequence.	
CD972346.1 GI:32832658	
EST.	
Zea mays	
ORGANISM	
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.	
1 (bases 1 to 430)	
Genopiante.	
Genopiante, a major partnership french program in plant genomics	
Unpublished (2003)	
Contact: Genopiante	
Genopiante	
93, rue Henri Rochefort 91025 EVRY CEDEX France	
Tel: 33 1 69 47 54 00	
Fax: 33 1 69 47 54 10	
This sequence has been generated in the framework of the french plant genomics programme 'Genopiante' (http://www.genopiante.com and http://genopiante-info.infobiogen.fr).	
Location/Qualifiers	
1..430	
/organism="Zea mays"	
/mol_type="mRNA"	
/cultivar="P2"	
/db_xref="taxon:4577"	
/clone="QAE20603"	
/tissue_type="pericarp"	
/clone_lib="QAE"	
Alignment Scores:	
Pred. No.:	430
Score:	1,26e-66
Percent Similarity:	600.50
Best Local Similarity:	98.37%
Query Match:	92.10%
Matches:	121
Conservative:	0
Mismatches:	0
Indels:	2

DB: 14 Gaps: 1

US-10-005-429-14 (1-126) x CD978907 (1-480)

QY 6 GlyAlaValIleAlaCysHisThrIysAspGluPheAspAlaArgMetAlaLysAlaLys 25

DB 3 GGTGGCGTGCATCGCGTCCACACCAAGGACGAGTTCGACGCCCGCATGCGCAAGCCCAAG 62

QY 26 GluGlnGlyLysLeuValIleAsp----PheValAlaProTyrCysSerGlyCysGln 44

DB 63 GAGCAGGGCAAGCTGTGTGTCATCGACGCTTCGATGCGCCCTCTGTGTCAGTGGTGCCA 122

QY 44 nMetMetAlaProValTyrAlaAspCysAlaSerLysTyrProSerAlaValPheLeuGln 64

DB 123 GATGATGGCCCGGTGTACCGGACTGCGCCAGGATACCTTCGCGGTCTTCTCTCGA 182

QY 64 uValAspValAspGluLeuGluValAlaLysIleTyrGlyValHisValMetProTh 84

DB 183 GGTGACGTCGACGAACTGCTGGAAGTTCGACGCTTCGCGGTCTGATGCGGAC 242

QY 84 rPheCysPheIleArgAsnGlyLysLeuGluSerPheAlaThrValAspGluAspGln 104

DB 243 CTCTCTCTTCATCAGGACGCGGAGGAGCTCGAGCTTGTCTACGTCGACGAGGACGA 302

QY 104 uLeuArgAspAlaValArgLysTyrAlaAlaGlyThrThrAlaProAlaSerAl 124

DB 303 GCTCCGGGACGGCTCAGGAAGTACGCCCGCTGCACTAGCAGCGCTCTGCTCGGC 362

QY 124 aSerAla 126

DB 363 GTCCGCC 369

RESULT 13

US-10-005-429-14 (1-126) x BG837151 (1-456)

QY 1 MetAlaAlaGluGluGlyAlaValIleAlaCysHisThrIysAspGluPheAspAlaArg 20

DB 369 ATGGCGCGCGAGGAGGGTGGCGGTGATCGCGTCCATACCAAGGACGAGTTCGACCCCGC 310

QY 21 MetAlaLysAlaLysGluGlnGlyLysLeuValIleAspPheMetAlaProTyrCys 40

DB 309 ATGGCCAAAGGCCCAAGGAGGAGGCAAGCTGTGGTTCATCGACTTCATGGCCCTGTGC 250

QY 41 SerGlyCysGlnMetMetAlaProValTyrAlaAspCysAlaSerLysTyrProSerAla 60

DB 249 AGTGGGTGCCAGATGATGCGCCCGTGTACCGGACTGCGGACGAGTACCTTCCCGC 190

QY 61 ValPheLeuGluValAspValAspGluLeuGluValAlaLysIleTyrGlyValHis 80

DB 189 GTCTTCCTCGAGTTCGACGCTCGAGCACTGCTGGAAGTTCGCGAGATCTACGGGTCCAT 130

QY 81 ValMetProThrPheCysPheIleArgAsnGlyLysLeuGluSerPheAlaThrVal 100

DB 129 GTGATGCGGACCTCTGCTTCATCAGGAACGCGGAGACGCTCGAGAGCTTTGCTACCGTC 70

QY 101 AspGluAspGluLeu-ArgAspAlaValArgLysTyrAlaAlaGlyThrThr 119

DB 69 GACGAGGACGAGCTHCCGCGACCGCTCGGAAGTACGACACGCGCTGGCAACTACA 12

RESULT 14

CF008093 426 bp mRNA linear EST 16-JUL-2003

OB17d05.xg QBI Zea mays cDNA clone QBI7d05, mRNA sequence.

CF008093

DEFINITION

CF008093.1 GI:32868411

VERSION

KEYWORDS

SOURCE

ORGANISM

Ze mays

Ze mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 456)

Harris,L.J., Balcerzak,M., Allard,S., Saparno,A., Couroux,P., De Moors,A., Hattori,J.I., Ouellet,T., Robert,L.S., Singh,J.A., Spratt,D. and Tinker,N.A.

Expressed Sequence Tags from Developing Maize Kernels Six Days after Silk Channel Inoculation with Fusarium graminearum

Unpublished (2001)

Contact: Harris, Linda J.

Eastern Cereal and Oilseed Research Centre

Agriculture and Agri-food Canada

Bldg. 21, Central Experimental Farm, Ottawa, Ontario, K1A 0C6, CANADA

Tel: (613) 759-1314

Fax: (613) 759-6566

Email: harrisl@em.agr.ca.

Location/Qualifiers

1. 456

/organism="Zea mays"

/mol_type="mRNA"

/cultivar="CO430"

/db_xref="taxon:4577"

/clone="Zm08_06b07"

/tissue_type="Developing kernels (sibcrossed)"

/dev_stage="10-11 days post-silk emergence"

/clone_1lib="Zm08_AAF_C_ECORC_Fusarium_graminearum_inoculate d_corn_ear"

/notes="Vector: Bluescript SK+/XhoI-EcoRI; Site_1: EcoRI;

FEATURES

source

1. 426

Location/Qualifiers

/organism="Zea mays"

/mol_type="mRNA"

/cultivar="F2"

/db_xref="taxon:4577"

/clone="QBI7d05"

/tissue_type="pedicel"

Site 2: XhoI; Field-grown maize ears were silk channel-inoculated in the morning (~10 am) with 1 ml of a Fusarium graminearum macroconidial suspension (500,000 spores/ml) and whole ears were collected and immediately frozen in liquid nitrogen 6 days later."

Alignment Scores:

Pred. No.: 5,89e-64 Length: 456

Score: 580.00 Matches: 114

Percent Similarity: 95.83% Conservative: 1

Best Local Similarity: 95.00% Mismatches: 4

Query Match: 88.96% Indels: 1

DB: 12 Gaps: 0

US-10-005-429-14 (1-126) x BG837151 (1-456)

QY 1 MetAlaAlaGluGluGlyAlaValIleAlaCysHisThrIysAspGluPheAspAlaArg 20

DB 369 ATGGCGCGCGAGGAGGGTGGCGGTGATCGCGTCCATACCAAGGACGAGTTCGACCCCGC 310

QY 21 MetAlaLysAlaLysGluGlnGlyLysLeuValIleAspPheMetAlaProTyrCys 40

DB 309 ATGGCCAAAGGCCCAAGGAGGAGGCAAGCTGTGGTTCATCGACTTCATGGCCCTGTGC 250

QY 41 SerGlyCysGlnMetMetAlaProValTyrAlaAspCysAlaSerLysTyrProSerAla 60

DB 249 AGTGGGTGCCAGATGATGCGCCCGTGTACCGGACTGCGGACGAGTACCTTCCCGC 190

QY 61 ValPheLeuGluValAspValAspGluLeuGluValAlaLysIleTyrGlyValHis 80

DB 189 GTCTTCCTCGAGTTCGACGCTCGAGCACTGCTGGAAGTTCGCGAGATCTACGGGTCCAT 130

QY 81 ValMetProThrPheCysPheIleArgAsnGlyLysLeuGluSerPheAlaThrVal 100

DB 129 GTGATGCGGACCTCTGCTTCATCAGGAACGCGGAGACGCTCGAGAGCTTTGCTACCGTC 70

QY 101 AspGluAspGluLeu-ArgAspAlaValArgLysTyrAlaAlaGlyThrThr 119

DB 69 GACGAGGACGAGCTHCCGCGACCGCTCGGAAGTACGACACGCGCTGGCAACTACA 12

RESULT 14

CF008093 426 bp mRNA linear EST 16-JUL-2003

OB17d05.xg QBI Zea mays cDNA clone QBI7d05, mRNA sequence.

CF008093

DEFINITION

CF008093.1 GI:32868411

VERSION

KEYWORDS

SOURCE

ORGANISM

Ze mays

Ze mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 426)

Genoplante,

Genoplante, a major partnership french program in plant genomics

Unpublished (2003)

Contact: Genoplante

Genoplante

93, rue Henri Rochefort 91025 EVRY CEDEX France

Tel: 33 1 69 47 54 00

Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (<http://www.genoplante.com>) and <http://genoplante-info.infobiogen.fr>.

Location/Qualifiers

1. 426

/organism="Zea mays"

/mol_type="mRNA"

/cultivar="F2"

/db_xref="taxon:4577"

/clone="QBI7d05"

/tissue_type="pedicel"

FEATURES

source

1. 426

Location/Qualifiers

/organism="Zea mays"

/mol_type="mRNA"

/cultivar="F2"

/db_xref="taxon:4577"

/clone="QBI7d05"

/tissue_type="pedicel"

/clone_lib="QBI"

ORIGIN

Alignment Scores:

Pred. No.: 2,7e-63 Length: 426
Score: 574.50 Matches: 116
Percent Similarity: 96.69% Conservatives: 1
Best Local Similarity: 95.87% Mismatches: 2
Query Match: 88.11% Indels: 2
DB: 14 Gaps: 1

US-10-005-429-14 (1-126) x CF008093 (1-426)

QY 1 MetAlaAlaGluGluGlyAlaValAlaCysHisThrLysAspGluPheAspAlaArg 20
DB 66 ATGGCGCCCGAGGAGGCTGCGGTGATCGCTGCCACCAAGGCGAGTTGCGAGCGCG 125
QY 21 MetAlaLysAlaLysGluGlnGlyLysLeuValValIleAspPhe-----MetAlaProTr 39
DB 126 ATGGCCCAAGCCCAAGGAGGCAAGCTGTTGTCATCGACTTCGGTCTATGSCCCCTG 185
QY 39 pCysSerGlyCysGlnMetMetAlaProValTyrAlaAspCysAlaSerLysTyrProSe 59
DB 186 GTGCAGTGGGTGCCAGATGATGCCCCGGTGATCGCGGATGCGCCAGCAAGTACCCCTC 245
QY 59 rAlaValPheLeuGluValAspValAspGluLeuLeuValAlaLysIleTyrGlyVa 79
DB 246 CGCGGTCTTCTCGAGTTCGAGTCGACGAACTGCTCGAAGTCGCGAAGATCTACGCGT 305
QY 79 lHisValMetProThrPheCysPheIleAsgGlnGlyGluThrLeuGluSerPheAlaTh 99
DB 306 CCATGTGATGCCGACCTTCCTGCTTCATCGGAACGGCGAGCGCTCGAGAGCTTTGCTAC 365
QY 99 rValAspGluAspGluLeuArgAspAlaValArgLysTyrAlaAlaGlyThrThrTh 119
DB 366 CTTGACGAGGACGAGCTCCGGACACCGCTCAGGAAGTCCGCCCGCGCTGGCACTAGGAC 425
QY 119 r 119
DB 426 G 426

RESULT 15

CF006552 QBI20e10.xg QBI Zea mays cDNA clone QBI20e10, mRNA sequence. EST 16-JUL-2003

LOCUS CF006552 573 bp mRNA linear EST 16-JUL-2003
DEFINITION QBI20e10.xg QBI Zea mays cDNA clone QBI20e10, mRNA sequence.
ACCESSION CF006552
VERSION CF006552.1 GI:32866870
KEYWORDS EST.
SOURCE Zea mays

ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 573)

REFERENCE Genoplante.
AUTHORS Genoplante, a major partnership french program in plant genomics
TITLE Unpublished (2003)
JOURNAL Contact: Genoplante
COMMENT Genoplante

93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (<http://www.genoplante.com>)
and <http://genoplante-info.inbio.fr>.

FEATURES

Location/Qualifiers
1..573
/organism="Zea mays"
/mol_type="mRNA"
/culivar="F2"
/db_xref="taxon:4577"
/clone="QBI20e10"
/tissue_type="pedicel"

/clone_lib="QBI"

ORIGIN

Alignment Scores:

Pred. No.: 2,46e-62 Length: 573
Score: 568.50 Matches: 123
Percent Similarity: 93.89% Conservatives: 0
Best Local Similarity: 93.89% Mismatches: 3
Query Match: 87.19% Indels: 5
DB: 14 Gaps: 1

US-10-005-429-14 (1-126) x CF006552 (1-573)

QY 1 MetAlaAlaGluGluGlyAlaValIleAlaCysHisThrLysAspGluPheAspAlaArg 20
DB 65 ATGGCGCCCGAGGAGGCTGCGGTGATCGGTGCCCAAGGACGAGTTGCGAGCGCGC 124
QY 21 MetAlaLysAlaLysGluGlnGlyLysLeuValValIleAsp-----PheMetAlaProTr 39
DB 125 ATGGCCCAAGGCCCAAGGAGGCAAGCTGGTGGTTCATCGACTTCGTTTATGGCCCCCTG 184
QY 39 pCysSerGlyCysGlnMetMetAlaProValTyrAlaAspCysAlaSerLysTyrProSe 59
DB 185 GTGCAGTGGGTGCCAGATGATGGCCCCGGGTGATCGCGGACTGGCCAGCAAGTACCCCTC 244
QY 59 rAlaValPheLeuGluValAspValAspGluLeuLeuValAlaLysIleTyrGlyVa 79
DB 245 CGCGGTCTTCTCGAGTTCGAGTCGACGACTGCTGGAAGTCCGGAAGATCTACGCGCT 304
QY 79 lHisValMetProThrPheCysPheIleAsgGlnGlyGluThrLeuGluSerPhe-Ala 99
DB 305 CCATGTGATGCCGACCTTCTGCTTCATCAGGAACGGCGAGAGCGCTCGAGAGCTTTGCTTA 364
QY 99 hrValAsp-GluAspGluLeuArg-AspAlaValArgLysTyrAlaAlaGlyThrTh 118
DB 365 CGGCGACGAGGACGAGCTCCGGGAGCGCGCTCAGGAAGTACGCGCGCGCTGGCACTAC 424
QY 118 rThrAlaProAlaSerAlaSerAla 126
DB 425 GACGGCTCTGCTCGCGGTTCGCGC 449

Search completed: May 5, 2004, 06:07:22

Job time : 1182.74 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 5, 2004, 03:14:43 ; Search time 36.3939 Seconds
(without alignments)
1921.307 Million cell updates/sec

Title: US-10-005-429-14
Perfect score: 652
Sequence: 1 MAABEGAVIACHTKDEPDAR.....DAVRKYAAGTTTAPASASA 126

Scoring table:

BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Rgapop 6.0, Rgapext 7.0
Delop 6.0, Delext 7.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+p2n.model -DRV=xlp
-Q=/cgn2_1/USPTO_spool_p/US10005429/runat_04052004_121650_15463/app.query.fasta_1.782
-DB=Issued Patents NA -Qfmt=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPEXT=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USFR=US10005429 -CGN 1 115 -runat 04052004_121650_15463 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSFLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents NA.*
1: /cgn2_6/ptodata/2/ina/5A COMB.seq.*
2: /cgn2_6/ptodata/2/ina/5B COMB.seq.*
3: /cgn2_6/ptodata/2/ina/6A COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B COMB.seq.*
5: /cgn2_6/ptodata/2/ina/pctus COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	315	48.3	466	4	US-09-621-976-1844
2	261	40.0	653	1	US-08-181-271A-103
3	261	40.0	653	1	US-08-449-315-103
4	261	40.0	653	1	US-08-444-803-103
5	261	40.0	653	1	US-08-449-043-103
6	261	40.0	653	1	US-08-456-265A-103
7	261	40.0	653	1	US-08-455-416-103
8	261	40.0	653	1	US-08-455-244-103
9	261	40.0	653	1	US-08-454-876-103
10	261	40.0	653	2	US-08-457-364-103
11	261	40.0	653	2	US-08-456-362-103
12	261	40.0	653	2	US-08-456-240-103

13	261	40.0	553	2	US-08-455-736-103	Sequence 103, App
14	261	40.0	553	2	US-08-971-217-103	Sequence 103, App
15	261	40.0	553	3	US-09-350-600-103	Sequence 103, App
16	261	40.0	553	4	US-09-906-234-103	Sequence 103, App
17	253	38.8	393	4	US-09-540-014-5	Sequence 5, Appli
18	251	38.5	369	4	US-09-540-014-1	Sequence 1, Appli
19	249	38.2	382	4	US-09-540-014-3	Sequence 3, Appli
20	232.5	35.7	318	4	US-09-313-294A-5868	Sequence 5868, Ap
21	208	31.9	278	4	US-09-313-294A-5840	Sequence 5840, Ap
22	178	27.3	557	4	US-09-404-879A-88	Sequence 88, Appl
23	178	27.3	557	4	US-09-338-933-88	Sequence 88, Appl
24	178	27.3	557	4	US-09-215-681-88	Sequence 88, Appl
25	178	27.3	557	4	US-09-215-003A-88	Sequence 88, Appl
26	178	27.3	581	4	US-09-601-144-67	Sequence 67, Appl
27	178	27.3	594	4	US-09-404-879A-87	Sequence 87, Appl
28	178	27.3	594	4	US-09-338-933-87	Sequence 87, Appl
29	178	27.3	594	4	US-09-215-681-87	Sequence 87, Appl
30	178	27.3	594	4	US-09-216-003A-87	Sequence 87, Appl
31	178	27.3	601	4	US-09-404-879A-133	Sequence 133, App
32	178	27.3	601	4	US-09-338-933-133	Sequence 133, App
33	178	27.3	601	4	US-09-215-681-133	Sequence 133, App
34	178	27.3	601	4	US-09-216-003A-133	Sequence 133, App
35	178	27.3	624	3	US-09-385-982-526	Sequence 526, App
36	178	27.3	630	3	US-08-180-371-5	Sequence 5, Appli
37	178	27.3	630	3	US-08-180-371-17	Sequence 17, Appl
38	178	27.3	630	5	PCT-US92-05707-5	Sequence 5, Appli
39	172	26.4	805	3	US-09-385-982-485	Sequence 485, App
40	161	24.7	2454	1	US-07-872-673B-1	Sequence 1, Appli
41	160.5	24.6	1545	1	US-07-872-673B-2	Sequence 2, Appli
42	160	24.5	631	3	US-09-385-982-174	Sequence 174, App
43	156.5	24.0	7096	4	US-09-221-017B-373	Sequence 373, App
44	154	23.6	1696	4	US-09-198-603C-3	Sequence 3, Appli
45	147.5	22.6	914	1	US-08-386-729A-9	Sequence 9, Appli

ALIGNMENTS

RESULT 1

US-09-621-976-1844
; Sequence 1844, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET 054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 1844
; LENGTH: 466
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 71..256
; NAME/KEY: sig peptide
; LOCATION: 71..199
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: score 4.30000019073486
; OTHER INFORMATION: seq VVIDFTAAACVHA/AP
US-09-621-976-1844

Alignment Scores:
Pred. No.: 1.58e-35
Score: 315.00
Percent Similarity: 69.05%
Best Local Similarity: 53.17%
Query Match: 48.31%
DB: 4
Length: 466
Matches: 67
Conservative: 20
Mismatches: 35
Indels: 5
Gaps: 1

Qy 42 GlyCysGlnMetMetAlaProValTyrAlaAspCysAlaSerLysTyrProSerAlaVal 61
Db 189 CTTGGCGTTTATTGCCCCCAATCTCTGTGACATTCCTAAGAGATGCCCATGTATA 248
Qy 62 PheLeuGluValAspValAspGluLeuLeuGluValAla-LysIleTyrGlyValHisVa 81
Db 249 TTCCTCAAGGTTGATGTGTGATGAACCTGAGACTGTTTCAGCGGAATGGAGTGGAGGC 308
Qy 81 lMetProThrPheCysPheIleArgAenGlyGluThrLeuGluSerPheAlaThrValAs 101
Db 309 AATGCCAATTTTGTCTTCTTATTAAGATGAAGAGAGTGCAGAGATGTTTGGTGCCTAA 368
Qy 101 pGluAspGluLeuArgAspAlaValArgLysTyrAlaAlaGlyThrThrAla 120
Db 369 GAAAGAGAGTTGCAGCAGACCATAGTGAAGCATGCTCTCTGCTACTGCTACTGCT 426

RESULT 3

US-08-449-315-103

; Sequence 103, Application US/08449315

; Patent No. 5650505

; GENERAL INFORMATION:

; APPLICANT: Ryals, John A.

; APPLICANT: Alexander, Danny C.

; APPLICANT: Beck, James J.

; APPLICANT: Duesing, John H.

; APPLICANT: Friedrich, Leslie B.

; APPLICANT: Goodman, Robert M.

; APPLICANT: Harms, Christian

; APPLICANT: Meins, Jr. Frederick

; APPLICANT: Montoya, Alice

; APPLICANT: Moyer, Mary B.

; APPLICANT: Neuhaus, Jean-Marc

; APPLICANT: Payne, George B.

; APPLICANT: Sperison, Christoph

; APPLICANT: Stinson, Jeffrey R.

; APPLICANT: Uknes, Scott J.

; APPLICANT: Ward, Eric R.

; APPLICANT: Williams, Shericea C.

; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC

; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF

; NUMBER OF SEQUENCES: 106

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CIBA-GEIGY Corporation

; STREET: 7 Skyline Drive

; CITY: Hawthorne

; STATE: New York

; COUNTRY: USA

; ZIP: 10532

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/449,315

; FILING DATE: 24-MAY-1995

; CLASSIFICATION: 800

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/181,271

; FILING DATE: 13-JAN-94

; APPLICATION NUMBER: US 08/093,301

; FILING DATE: 16-JUL-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/937,197

; FILING DATE: 6-NOV-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/678,378

; FILING DATE: 1-APR-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/305,566

; FILING DATE: 6-FEB-1989

; PRIOR APPLICATION DATA:

; PRIOR APPLICATION DATA:

; PRIOR APPLICATION DATA:

; PRIOR APPLICATION DATA:

; PRIOR APPLICATION DATA:

; PRIOR APPLICATION DATA:

; PRIOR APPLICATION DATA:

; PRIOR APPLICATION DATA:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/165,667
; FILING DATE: 8-MAR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/042,847
; FILING DATE: 6-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/632,441
; FILING DATE: 21-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/425,504
; FILING DATE: 20-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/848,506
; FILING DATE: 6-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/768,122
; FILING DATE: 27-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/580,431
; FILING DATE: 7-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/368,672
; FILING DATE: 20-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/329,018
; FILING DATE: 24-MAR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/045,957
; FILING DATE: 12-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: S-19825/PI/CGC 1727
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8614
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 103:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 653 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-449-315-103

Alignment Scores:
Pred. No.: 118e-27 Length: 653
Score: 261.00 Matches: 51
Percent Similarity: 62.50% Conservative: 24
Best Local Similarity: 42.50% Mismatches: 44
Query Match: 40.03% Indels: 1
DB: 1 Gaps: 0

US-10-005-429-14 (1-126) x US-08-449-315-103 (1-653)
Qy 2 AlaAlaGluGluGlyAlaValIleAlaCysHisThrLysAspGluPheAspAlaArgMet 21
Db 69 TCATCCGAGGAGGACAAAGTGTTCGGCTGCCACAAAGTTTCAGGAATGGAACGAGTACTTC 128
Qy 22 AlaLysAlaLysGluGlnGlyLysLeuValIleAspPheMetAlaProTyrCysSer 41
Db 129 AAGAAAGCGCTTGAGACTAAGAAACCTGGTGGTGCATTTACTGCTTCATGCTGGCGGS 188
Qy 42 GlyCysGlnMetMetAlaProValTyrAlaAspCysAlaSerLysTyrProSerAlaVal 61
Db 189 CCTTCCGCTTTTATTGCCCCCAATCTCTGTGACATTCCTAAGAGATGCCCATGTATA 248
Qy 62 PheLeuGluValAspValAspGluLeuLeuGluValAla-LysIleTyrGlyValHisVa 81
Db 249 TTCCTCAAGGTTGATGTGTGATGAACCTGAGACTGTTTCAGCGGAATGGAGTGGAGGC 308
Qy 81 lMetProThrPheCysPheIleArgAenGlyGluThrLeuGluSerPheAlaThrValAs 101

Db 309 AATGCCAACTTTGCTTCATTAAAGTGGAAAGAGTGGACAGAGTTGTTGGTCCAA 368
QY 101 pGluaspGluLeuAargAspAlaValaLgLyTyAlaAlaGlyThrThrAla 120
Db 369 GAAAGAGAGTTTGACGACGACCATAGTGAAGCATGTGCTCTGCTACTGTCTGCT 426

RESULT 4

US-08-444-803-103
; Sequence 103 Application US/08444803
; Patent No. 5654414

GENERAL INFORMATION:

; APPLICANT: Ryals, John A.
; APPLICANT: Alexander, Danny C.
; APPLICANT: Beck, James J.
; APPLICANT: Duesing, John H.
; APPLICANT: Friedrich, Leslie B.
; APPLICANT: Goodman, Robert M.
; APPLICANT: Harms, Christian
; APPLICANT: Melns, Jr., Frederick
; APPLICANT: Montoya, Alice
; APPLICANT: Moyer, Mary B.
; APPLICANT: Neuhaus, Jean-Marc
; APPLICANT: Payne, George B.
; APPLICANT: Sperison, Christoph
; APPLICANT: Stinson, Jeffrey R.
; APPLICANT: Uknes, Scott J.
; APPLICANT: Ward, Eric R.
; APPLICANT: Williams, Shericea C.
; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,803
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/181,271
; FILING DATE: 13-JAN-94
; APPLICATION NUMBER: US 08/093,301
; FILING DATE: 16-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/937,197
; FILING DATE: 6-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/678,378
; FILING DATE: 1-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/305,566
; FILING DATE: 6-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/165,667
; FILING DATE: 8-MAR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/042,847
; FILING DATE: 6-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/632,441
; FILING DATE: 21-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/425,504
; FILING DATE: 20-OCT 1989

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/848,506
; FILING DATE: 6-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/768,122
; FILING DATE: 27-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/580,431
; FILING DATE: 7-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/368,672
; FILING DATE: 20-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/329,018
; FILING DATE: 24-MAR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/045,957
; FILING DATE: 12-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8614
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 103:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 653 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-444-803-103

Alignment Scores:

Pred. No.: 1.18e-27 Length: 653
Score: 261.00 Matches: 51
Percent Similarity: 62.50% Conservative: 24
Best Local Similarity: 42.50% Mismatches: 44
Query Match: 40.03% Indels: 1
DB: 1 Gaps: 0

US-10-005-429-14 (1-126) x US-08-444-803-103 (1-653)

QY 2 AlaAlaGluGluGlyAlaValIleAlaCysHisThrLysAspGluPheAspAlaArgMet 21
Db 69 TCATCCGAGGAGGAGGACAAAGTGTTCGGCTGCCACCAAGTTGAGGAGTGAACGAGTACTTC 128
QY 22 AlalysAlalysGluGlnGlyLysLeuValValIleAspPheMetAlaProTyrCysSer 41
Db 129 AAGAAAGCGGTGTGAGACTAAGAACTGGTGGTGGTATTTTACTGCTTCATGCTGCGGS 188
QY 42 GlyCysGlnMetMetAlaProValTyrAlaAspCysAlaSerLysTyrProSerAlaVal 61
Db 189 CCTTGGCGTTTATTGCCCCCAATTCCTGCTGACATTGCTAAGAGAGATGCCCATGTTATA 248
QY 62 PheLeuGluValAspValAspGluLeuGluValAlaLysIleTyrGlyValHisVa 81
Db 249 TTCTCAAGGTTCATGTTGATGAACCTGTTTTCAGCGGGAATGAGTGTGGAGGC 308
QY 81 lMetProThrPheCysPheIleAargAsnGlyGluThrLeuGluSerPheAlaThrValas 101
Db 309 AATGCCAACTTTGCTTCATTAAAGATGAAAGAGTGGACAGAGTTGTTGGTCCAA 368
QY 101 pGluaspGluLeuAargAspAlaValaLgLyTyAlaAlaGlyThrThrAla 120
Db 369 GAAAGAGAGTTTGACGACGACCATAGTGAAGCATGTGCTCTGCTACTGTCTGCT 426

RESULT 5

US-08-449-043-103
; Sequence 103 Application US/08449043
; Patent No. 5689044
; GENERAL INFORMATION:

APPLICANT: Ryals, John A.
 APPLICANT: Alexander, Danny C.
 APPLICANT: Beck, James J.
 APPLICANT: Duesing, John H.
 APPLICANT: Friedrich, Leslie B.
 APPLICANT: Goodman, Robert M.
 APPLICANT: Harms, Christian
 APPLICANT: Meins, Jr., Frederick
 APPLICANT: Montoya, Alice
 APPLICANT: Moyer, Mary B.
 APPLICANT: Neuhaus, Jean-Marc
 APPLICANT: Payne, George B.
 APPLICANT: Sperison, Christoph
 APPLICANT: Stinson, Jeffrey R.
 APPLICANT: Uknes, Scott J.
 APPLICANT: Ward, Eric R.
 APPLICANT: Williams, Shericca C.
 TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
 TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
 NUMBER OF SEQUENCES: 106
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: CIBA-GEIGY Corporation
 STREET: 7 Skyline Drive
 CITY: Hawthorne
 STATE: New York
 COUNTRY: USA
 ZIP: 10532
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/449,043
 FILING DATE: 24-MAY-1995
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/181,271
 FILING DATE: 13-JAN-94
 APPLICATION NUMBER: US 08/093,301
 FILING DATE: 16-JUL-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/937,197
 FILING DATE: 6-NOV-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/678,378
 FILING DATE: 1-APR-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/305,566
 FILING DATE: 6-FEB-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/165,667
 FILING DATE: 8-MAR-1988
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/042,847
 FILING DATE: 6-APR-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/632,441
 FILING DATE: 21-DEC-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/425,504
 FILING DATE: 20-OCT-1985
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/848,506
 FILING DATE: 6-MAR-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/768,122
 FILING DATE: 27-SEP-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/580,431
 FILING DATE: 7-SEP-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/368,672

FILING DATE: 20-JUN-1989
 PRIOR APPLICATION DATA: US 07/329,018
 FILING DATE: 24-MAR-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/045,957
 FILING DATE: 12-APR-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Elmer, James Scott
 REGISTRATION NUMBER: 36,129
 REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (919)541-8614
 TELEFAX: (919)541-8689
 INFORMATION FOR SEQ ID NO: 103:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 653 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-449-043-103
 Alignment Scores:
 Pred. No.: 1.18e-27 Length: 653
 Score: 261.00 Matches: 51
 Percent Similarity: 62.50% Conservative: 24
 Best Local Similarity: 42.50% Mismatches: 44
 Query Match: 40.03% Indels: 1
 DB: 0
 US-10-005-429-14 (1-126) x US-08-449-043-103 (1-653)
 Qy 2 AlaAlaGluGluGlyAlaValIleAlaCysHisThrLysAspGluPheAspAlaArgMet 21
 Db 69 TCATCCGAGGAGGAGGACAGTGTTCGGCTGCCACAGGTTGAGGAAATGGAACGAGTACTTC 128
 Qy 22 AlaLysAlaLysGluGlnGlyLysLeuValIleAspPheMetAlaProTyrCysSer 41
 Db 129 AAGAAAGCGCGTTCAGACTTAAGAAACTGGTGTGTGCGATTTTACTGCTTCATGCTGCGGS 189
 Qy 42 GlyCysGlnMetMetAlaProValTyrAlaAspCysAlaSerLysTyrProSerAlaVal 61
 Db 189 CTTGCGGTTTATTCGCCCAATCTTCTGACATGCTAAGAGATGCCCAATGTTATA 248
 Qy 62 PheLeuGluValAspValAspGluLeuGluValAlaLysIleTyrGlyValHisVa 81
 Db 249 TTCTCAAGGTTGATGTTGATGAACCTGATGACTGTTTTCAGCGGGAATGGAGTGTGGAGC 308
 Qy 81 lMetProThrPheCysPheIleArgGlnGlyGluThrLeuGluSerPheAlaThrValas 101
 Db 309 AATGCCCACTTTTGTCTTCATTAAAGATGAAAGAGTGGACAGAGTGTGTGGTGCACAA 368
 Qy 101 pGluAspGluLeuArgAspAlaValArgLysTyrAlaAlaGlyThrThrAla 120
 Db 369 GAAAGAGGAGTTCGACGACAGCACCATTAGTAGAGCATGCTCTCTCTACTGTCTACTGCT 426
 RESULT 6
 US-08-456-265A-103
 Sequence 103, Application US/08456265A
 Patent No. 5767369
 GENERAL INFORMATION:
 APPLICANT: Alexander, Danny C.
 APPLICANT: Ryals, John A.
 APPLICANT: Goodman, Robert M.
 APPLICANT: Stinson, Jeffrey R.
 TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
 TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
 NUMBER OF SEQUENCES: 111
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: CIBA-GEIGY Corporation
 STREET: 520 White Plains Road, P.O. Box 2005
 CITY: Tarrytown

STATE: New York
COUNTRY: USA
ZIP: 10591
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,265A
FILING DATE: 31-MAY-95
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/181,271
FILING DATE: 13-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Weigs, J. Timofky
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727/DIV10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 103:
SEQUENCE CHARACTERISTICS:
LENGTH: 653 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-456-265A-103

Alignment Scores:
Pred. No.: 1,18e-27 Length: 653
Score: 261.00 Matches: 51
Percent Similarity: 62.50% Conservative: 24
Best Local Similarity: 42.50% Mismatches: 44
Query Match: 40.03% Indels: 1
DB: Gaps: 0
US-10-005-429-14 (1-126) x US-08-456-265A-103 (1-653)
QY 2 AlaAlaGluGluGlyAlaValIleAlaCysHisThrLysAspGluPheAspAlaArgMet 21
DB 69 TCATCCGAGGAGGACAAAGTTCGGCTGCCCAAGTTGAGGAATGGAACGAGTACTTC 128
QY 22 AlaAlaAlaLysGluGluGlnGlyLysLeuValIleAspPheMetAlaProTyrCysSer 41
DB 129 AAGAAAGCGCTTGAGACTAGAAACTGGTGGTGCATTTTACTGCTTCATGGTGGG 188
QY 42 GlyCysGlnMetMetAlaProValTyrAlaAspCysAlaSerLysTyrProSerAlaVal 61
DB 189 CTTTGGCGTTTATTGCCCCCAATTCTTGTGACATTGCTAAGAGATGCCCCCATGTTATA 249
QY 62 PheLeuGluValAspValAspGluLeuGluValAla-LysIleTyrGlyValHisVa 81
DB 249 TTCTCAAGGTTCATGTTGATGAACCTGAAGACTGTTTCAGCGGAATGGAGTGGAGGC 308
QY 81 lMetProThrPheCysPheIleArgAsnGlyGluThrLeuGluSerPheAlaThrValAs 101
DB 309 AATGCCAACTTTTGTCTTTCATTAAAGATGAAAGAGTGGACAGAGTGTGTGTGCCAA 368
QY 101 pGluAspGluLeuArgAspAlaValArgLysTyrAlaAlaAlaGlyThrThrAla 120
DB 369 GAAAGAGGNGTTGCAGCAGACCATAGTGAAGCATGCTGCTCTCTCTACTGCTGCT 426
RESULT 7
US-08-455-416-103
Sequence 103, Application US/08455416
Patent No. 5777200
GENERAL INFORMATION:
APPLICANT: Ryals, John A.
APPLICANT: Alexander, Danny C.
APPLICANT: Beck, James J.
APPLICANT: Duesing, John H.
APPLICANT: Friedrich, Leslie B.
APPLICANT: Goodman, Robert M.
APPLICANT: Harms, Christian
APPLICANT: Meins, Jr., Frederick
APPLICANT: Montoya, Alice
APPLICANT: Moyer, Mary B.
APPLICANT: Neuhaus, Jean-Marc
APPLICANT: Payne, George B.
APPLICANT: Sperison, Christoph
APPLICANT: Stinson, Jeffrey R.
APPLICANT: Uknes, Scott J.
APPLICANT: Ward, Eric R.
APPLICANT: Williams, Shericca C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,416

```

; FILING DATE: 31-MAY-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/181,271
; FILING DATE: 13-JAN-94
; APPLICATION NUMBER: US 08/093,301
; FILING DATE: 16-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/937,197
; FILING DATE: 6-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/678,378
; FILING DATE: 1-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/305,566
; FILING DATE: 6-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/165,667
; FILING DATE: 8-MAR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/042,847
; FILING DATE: 6-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/632,441
; FILING DATE: 21-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/425,504
; FILING DATE: 20-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/848,506
; FILING DATE: 6-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/768,122
; FILING DATE: 27-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/580,431
; FILING DATE: 7-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/368,672
; FILING DATE: 20-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/329,018
; FILING DATE: 24-MAR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/045,957
; FILING DATE: 12-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/POCKET NUMBER: S-19825/P1/CGC 1727
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8614
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 103:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 653 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-455-416-103

Alignment Scores:
Pred. No.: 1,19e-27 Length: 653
Score: 261.00 Matches: 51
Percent Similarity: 62.50% Conservative: 24
Best Local Similarity: 42.50% Mismatches: 44
Query Match: 40.03% Indels: 1
DB: 1 Gaps: 0

US-10-005-429-14 (1-126) x US-08-455-416-103 (1-653)

Qy 2 AlaalaGluGluGlyAlaValIleAlaCysHisThrIysAspGluPheAspAlaArgMet 21

```

```

Db 69 TCATCCGAGGAGGCAAGTGTTCGGCTGCCCAAGGTTGAGCAATGGAACGAGTACTTC 128
Qy 22 AlaLysAlaLysGluGlnGlyValLeuValIleAspPheMetAlaProTyrCysSer 41
Db 129 AAGAAAGGGGTGAGACTAAGAAACCTGGTGCTGCTGATTTACTGCTTCATGTTGGG 188
Qy 42 GlyCysGlnMetMetAlaProValTyrAlaAspCysAlaSerLysTyrProSerAlaVal 61
Db 189 CCTTGGCGTTTATTGCCCCCAATCTTGTGACATTGCTAAGAGATGCCCCCATGTTATA 248
Qy 62 PheLeuGluValAspValAspGluLeuValAla-LysIleTyrGlyValHisVa 81
Db 249 TTCTCAAGGTTGATGTTGATGAACCTGTTTCAGCGGGAATGGAGTGTGGAGGC 308
Qy 81 lMetProThrPheCysPheIleArgAsnGlyGluThrLeuGluSerPheAlaThrValas 101
Db 309 AATGCCACCTTTTGTCTTCAATTAAGATGGAAGAAGTGGACAGAGTTGTTGGTGCAA 368
Qy 101 pGluAspGluLeuArgAspAlaValargLysTyrAlaAlaGlyThrThrAla 120
Db 369 GAAAGAGGAGTTGCAGCAGACCATAGTGAAGCATGCTCTCTACTGCTACTGCT 426

RESULT 8
US-08-455-244-103
; Sequence 103, Application US/08455244
; Patent No. 5783214
; GENERAL INFORMATION:
; APPLICANT: Ryals, John A.
; APPLICANT: Alexander, Danny C.
; APPLICANT: Beck, James J.
; APPLICANT: Duesing, John H.
; APPLICANT: Friedrich, Leslie B.
; APPLICANT: Goodman, Robert M.
; APPLICANT: Harms, Christian
; APPLICANT: Meins, Jr., Frederick
; APPLICANT: Montoya, Alice
; APPLICANT: Moyer, Mary B.
; APPLICANT: Neuhaus, Jean-Marc
; APPLICANT: Payne, George B.
; APPLICANT: Sperison, Christoph
; APPLICANT: Stinson, Jeffrey R.
; APPLICANT: Uknes, Scott J.
; APPLICANT: Ward, Eric R.
; APPLICANT: Williams, Shericca C.
; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/455,244
; FILING DATE: 31-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/181,271
; FILING DATE: 13-JAN-94
; APPLICATION NUMBER: US 08/093,301
; FILING DATE: 16-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/937,197
; FILING DATE: 6-NOV-1992
; PRIOR APPLICATION DATA:

```

```

1 APPLICATION NUMBER: US 07/678,378
2 FILING DATE: 1-APR-1991
3 PRIOR APPLICATION DATA:
4 APPLICATION NUMBER: US 07/305,566
5 FILING DATE: 6-FEB-1989
6 PRIOR APPLICATION DATA:
7 APPLICATION NUMBER: US 07/165,667
8 FILING DATE: 8-MAR-1988
9 PRIOR APPLICATION DATA:
10 APPLICATION NUMBER: US 08/042,847
11 FILING DATE: 6-APR-1993
12 PRIOR APPLICATION DATA:
13 APPLICATION NUMBER: US 07/632,441
14 FILING DATE: 21-DEC-1990
15 PRIOR APPLICATION DATA:
16 APPLICATION NUMBER: US 07/425,504
17 FILING DATE: 20-OCT-1989
18 PRIOR APPLICATION DATA:
19 APPLICATION NUMBER: US 07/848,506
20 FILING DATE: 6-MAR-1992
21 PRIOR APPLICATION DATA:
22 APPLICATION NUMBER: US 07/768,122
23 FILING DATE: 27-SEP-1991
24 PRIOR APPLICATION DATA:
25 APPLICATION NUMBER: US 07/580,431
26 FILING DATE: 7-SEP-1990
27 PRIOR APPLICATION DATA:
28 APPLICATION NUMBER: US 07/368,672
29 FILING DATE: 20-JUN-1989
30 PRIOR APPLICATION DATA:
31 APPLICATION NUMBER: US 07/329,018
32 FILING DATE: 24-MAR-1989
33 PRIOR APPLICATION DATA:
34 APPLICATION NUMBER: US 08/045,957
35 FILING DATE: 12-APR-1993
36 ATTORNEY/AGENT INFORMATION:
37 NAME: Elmer, James Scott
38 REGISTRATION NUMBER: 36,129
39 REFERENCE/DOCKET NUMBER: S-19825/1
40 TELECOMMUNICATION INFORMATION:
41 TELEPHONE: (919)541-8614
42 TELEFAX: (919)541-8689
43 INFORMATION FOR SEQ ID NO: 103:
44 SEQUENCE CHARACTERISTICS:
45 LENGTH: 653 base pairs
46 TYPE: nucleic acid
47 STRANDEDNESS: single
48 TOPOLOGY: linear
49 MOLECULE TYPE: DNA (genomic)
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918

```

Alignment Scores:		
Pred. No.:	1.19E-27	Length:
Score:	261.00	Matches:
Percent Similarity:	62.50%	Conservative:
Best Local Similarity:	42.50%	Mismatches:
Query Match:	40.03%	Indels:
DB:	1	Gaps:
		553
		51
		24
		44
		0
		0

US-10-005-429-14 (1-126) X US-08-455-244-103 (1-653)

QY	2	AlaAlaGluGluGlyAlaVal	AlaCysHisThrLysAspGluPheAspAlaArgMet	21
DB	69	TCATCCGAGGAGGACAAGTTCGGCTGCCACAAAGGTTGAGGAATGGAACGAGTAGTACTTC		128
QY	22	AlaLysAlaLysGluGlnGlyLysLeuValValLysPheMetAlaProThrCysSer	41	
DB	129	AAGAAAGGGGTTTGAGACTAAGAAACTGGTGGTGGTCAATTTACTGCTTCATGGTGGGS		188
QY	42	GlyCysGlnMetMetAlaProValTyrAlaAspCysAlaSerLysTyrProSerAlaVal	61	
DB	189	CCTTGGCGTTTATTCGCCCAATCTTGCTGACATTCGTAAAGAAGATGCCCATGTATTA		248

```

QY      62 PheLeuGluValAspValaspGluLeuGluValAla-LysIleTyrGlyValHisVa 81
Db      249 TTCTCAGGTTTGATGTTGAGTCACTGACACTGTTTCAGCGGAGTGGAGTGTGGAGC 308
QY      81 lmetProThrPheCysPheIleArgAsnGlyGluThrLeuGluSerPheAlaThrValas 101
Db      309 AATGCCAACTTTTGTCTTCATTAAAGATGGAAGAAGTGCACAGAGTGTGTGGTGC 368
QY      101 pGluAspGluLeuArgAspAlaValArgLysTyrAlaAlaGlyThrThrAla 120
Db      369 GAAAGAGGAGTTTCAGCAGACACCTAGTGAAGCATGCTGCTCTCTACTGTCTCT 426

RESULT 9
US-08-454-876-103
; Sequence 103, Application US/08454876
; Patent No. 5804693
; GENERAL INFORMATION:
; APPLICANT: Ryals, John A.
; APPLICANT: Alexander, Danny C.
; APPLICANT: Beck, James J.
; APPLICANT: Duesing, John H.
; APPLICANT: Friedrich, Leslie B.
; APPLICANT: Goodman, Robert M.
; APPLICANT: Harms, Christian
; APPLICANT: Meins, Jr., Frederick
; APPLICANT: Montoya, Alice
; APPLICANT: Moyer, Mary B.
; APPLICANT: Neuhaus, Jean-Marc
; APPLICANT: Payne, George B.
; APPLICANT: Sperison, Christoph
; APPLICANT: Stinson, Jeffrey R.
; APPLICANT: Uknes, Scott J.
; APPLICANT: Ward, Eric R.
; APPLICANT: Williams, Shericca C.
; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
; NUMBER OF INVENTION: DNA SEQUENCES AND USES THEREOF
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/454,876
; FILING DATE: 31-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/181,271
; FILING DATE: 13-JAN-94
; APPLICATION NUMBER: US 08/093,301
; FILING DATE: 16-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/937,197
; FILING DATE: 6-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/678,378
; FILING DATE: 1-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/305,566
; FILING DATE: 6-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/165,567
; FILING DATE: 8-MAR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/042,847
; FILING DATE: 6-APR-1993

```

PRIOR APPLICATION DATA: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA: US 07/425,504
FILING DATE: 20-OCT-1989
PRIOR APPLICATION DATA: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA: US 07/768,122
FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA: US 07/580,431
FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATA: US 07/368,672
FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-19825/PI/CGC 1727
TELEPHONE: (919)541-8614
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 103:
SEQUENCE CHARACTERISTICS:
LENGTH: 653 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-454-876-103

Alignment Scores:
Pred. No.: 1,18e-27 Length: 653
Score: 261.00 Matches: 51
Percent Similarity: 62.50% Conservative: 24
Best Local Similarity: 42.50% Mismatches: 44
Query Match: 40.03% Indels: 1
DB: 1 Gaps: 0

US-10-005-429-14 (1-126) x US-08-454-876-103 (1-653)

Qy 2 AlaAlaGluGluGlyAlaValIleAlaCysHisThrLysAspGluPheAspAlaArgMet 21
TCTTCGAGGAGGACGACGAGTTCGCTGCCACAGGTTGAGGATGGACGAGTACTTC 128
Db 69 TCAICGAGGAGGACGACGAGTTCGCTGCCACAGGTTGAGGATGGACGAGTACTTC 128

Qy 22 AlaAlaGluGluGlyAlaValIleAlaCysHisThrLysAspGluPheAspAlaArgMet 41
TCTTCGAGGAGGACGACGAGTTCGCTGCCACAGGTTGAGGATGGACGAGTACTTC 188
Db 129 AAGAAGGCGTTCGAGACTAAGAACTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 188

Qy 42 GlyCysGlnMetMetAlaProValTyrAlaAspCysHisThrLysAspGluPheAspAlaArgMet 61
TCTTCGAGGAGGACGACGAGTTCGCTGCCACAGGTTGAGGATGGACGAGTACTTC 248
Db 189 CCTTGGCGTTTATGTCCTTATGTCCTTATGTCCTTATGTCCTTATGTCCTTATG 248

Qy 62 PheLeuGluValAspValAspGluLeuGluValAlaLysIleTyrGlyValHisVa 81
TCTTCGAGGAGGACGACGAGTTCGCTGCCACAGGTTGAGGATGGACGAGTACTTC 308
Db 249 TTCTCAAGGTTGATGTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 308

Qy 81 lMetProThrPheCysPheIleArgAsnGlyGluThrLeuGluSerPheAlaThrValAs 101
TCTTCGAGGAGGACGACGAGTTCGCTGCCACAGGTTGAGGATGGACGAGTACTTC 368
Db 309 AATGCCAACATTTTCTCTCTTATTAAGATGAAGATGAAGATGAAGATGAAGATGAAG 368

Qy 101 pGluAspGluLeuArgAspAlaValAspGlyTyrAlaAlaGlyThrThrAla 120
TCTTCGAGGAGGACGACGAGTTCGCTGCCACAGGTTGAGGATGGACGAGTACTTC 426
Db 369 GAAAGAGGAGTTCGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 426

RESULT 10
US-08-457-364-103
Sequence 103, Application US/08457364
Patent No. 5847258
GENERAL INFORMATION:
APPLICANT: Ryals, John A.
APPLICANT: Alexander, Danny C.
APPLICANT: Beck, James J.
APPLICANT: Duesing, John H.
APPLICANT: Friedrich, Leslie B.
APPLICANT: Goodman, Robert M.
APPLICANT: Harms, Christian
APPLICANT: Meins, Jr., Frederick
APPLICANT: Montoya, Alice
APPLICANT: Moyer, Mary B.
APPLICANT: Neuhaus, Jean-Marc
APPLICANT: Payne, George B.
APPLICANT: Sperison, Christoph
APPLICANT: Stinson, Jeffrey R.
APPLICANT: Unnes, Scott J.
APPLICANT: Ward, Eric R.
APPLICANT: Williams, Shericca C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSER: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,364
FILING DATE: 31-MAY-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/181,271
FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
APPLICATION NUMBER: US 07/768,122

APPLICANT: Williams, Shericca C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
DNA SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIRA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM: disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,240
FILING DATE: 31-MAY-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/181,271
FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 103:
SEQUENCE CHARACTERISTICS:

Alignment Scores:
Pred. No.: 1,18e-27 Length: 653
Score: 261.00 Matches: 51
Percent Similarity: 62.50% Conservative: 24
Best Local Similarity: 42.50% Mismatches: 44
Query Match: 40.03% Indels: 1
DB: 2 Gaps: 0

US-10-005-429-14 (1-126) x US-08-456-262-103 (1-653)

QY 2 AlaAlaGluGluGlyAlaValAlaCysHisThrLysAspGluPheAspAlaArgMet 21
Db 69 TCATCCGAGGAGGAGCAAGTTCGGTCCGACAGGTGGAGGATGGAGGATCTTC 128
QY 22 AlaLysAlaLysGluGlnGlyLysLeuValValLleAspPheMetAlaProTyrCysSer 41
Db 129 AAGAAGCGCGTTGAGACTAAGAACTGCTGGTGGTTCGATTCTGCTTCATGCTGGG 188
QY 42 GlyCysGlnMetMetAlaProValTyrAlaAspCysAlaSerLysTyrProSerAlaVal 61
Db 189 CATTGCCGCTTTATTTGCCCAATCTTCTGACATGCTAAGAGAGTCCCATGTTATA 248
QY 62 PheLeuGluValAspValAspGluLeuGluValAlaLysIleTyrGlyValHisVa 81
Db 249 TTCTCTCAAGTTGATGTTGATGATGATGATGATGATGATGATGATGATGATGATG 308
QY 81 LmetProThrPheCysPheIleArgAsnGlyGluThrLeuGluSerPheAlaThrValas 101
Db 309 AATGCCAACTTTGCTTCTTCAATTAAGATGGAAGAGTGGACAGAGTTGTTGGTGC 368
QY 101 pGluAspGluLeuArgAspAlaValArgLysTyrAlaAlaGlyThrThrAla 120
Db 369 GAAGAGGAGTTGACAGACACCAATGAGCAATGCTCTCTGCTACTGCTACTGCT 426

RESULT 12

US-08-456-240-103
Sequence 103, Application US/08456240
Patent No. 5856154

GENERAL INFORMATION:

APPLICANT: Ryals, John A.
APPLICANT: Alexander, Danny C.
APPLICANT: Beck, James J.
APPLICANT: Duesing, John H.
APPLICANT: Friedrich, Leslie B.
APPLICANT: Goodman, Robert M.
APPLICANT: Harms, Christian
APPLICANT: Meins, Jr., Frederick
APPLICANT: Montoya, Alice
APPLICANT: Neuhau, Jean-Marc
APPLICANT: Payne, George B.
APPLICANT: Sperison, Christoph
APPLICANT: Stinson, Jeffrey R.
APPLICANT: Uknes, Scott J.
APPLICANT: Ward, Eric R.


```

Best Local Similarity: 42.50% Mismatches: 44
Query Match: 40.03% Indels: 1
DB: 2 Gaps: 0

US-10-005-429-14 (1-126) x US-08-455-736-103 (1-653)

Qy 2 AlaAlaGluGluGluGluValValIleAlaCysHisThrLysAspGluPheAspAlaArgMet 21
Db 69 TCATCCGAGGAGGACAAAGTGTTCGGCTGCCCAAGGTTGAGGAATGGAACGAGTACTTC 128
Qy 22 AlaLysAlaLysGluGlnGlyLysLeuValValIleAspPheMetAlaProTTPCySer 41
Db 129 AAGAAAGGCGTTGAGACTAAGAACTGGTGGTGGTTCGATTTTACTGCTTCATGTCGGGS 188
Qy 42 GlyCysGlnMetMetAlaProValTyAlaLysCysAlaSerLysTyrProSerAlaVal 61
Db 189 CCTTGGCGTTTATTGGCCCAATCTTGTGACATGCTAAGAAAGCCCATGTTTATA 248
Qy 62 PheLeuGluValAspValAspGluLeuLeuGluValAlaLysIleTyrGlyValHisVa 81
Db 249 TTCTCAAGTTGATGTTGATGACTGAAGACTGTTTCAGCGGGAATGGAGTGTGGAGGC 308
Qy 81 lMetProThrPheCysPheIleArgAsnGlyGluThrLeuGluSerPheAlaThrValAs 101
Db 309 AATGCCAACTTTGTCTTCATTAAAGATGGAAGAGTGGACAGAGTTGTTGTGCCAA 368
Qy 101 pGluAspGluLeuValAspAlaValAlaGlyIleValAlaGlyThrThrAla 120
Db 369 GAAAGAGGAGTTGCACACAGACCATGATGAGGATGCTGCTCTGCTACTGCTGCT 426

RESULT 14
US-08-971-217-103
: Sequence 103, Application US/08971217
: Patent No. 5942662
: GENERAL INFORMATION:
: APPLICANT: Ryals, John A.
: APPLICANT: Harms, Christian
: APPLICANT: Friedrich, Leslie
: APPLICANT: Beck, James
: APPLICANT: Uknes, Scott
: APPLICANT: Ward, Eric
: TITLE OF INVENTION: INDUCIBLE HERBICIDE RESISTANCE
: NUMBER OF SEQUENCES: 111
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: No. 5942662artis Corporation
: STREET: 3054 Cornwallis Road, P.O. Box 12257
: CITY: Research Triangle Park
: STATE: NC
: COUNTRY: USA
: ZIP: 27709
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/971,217
: FILING DATE:
: CLASSIFICATION: 800
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/457,364
: FILING DATE: 31-MAY-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/181,271
: FILING DATE: 13-JAN-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/093,301
: FILING DATE: 16-JUL-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/937,197
: FILING DATE: 6-NOV-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/678,378

FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/355,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/142,847
FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/648,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/358,122
FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/390,431
FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/358,672
FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/645,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727/DIV5/CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 103:
SEQUENCE CHARACTERISTICS:
LENGTH: 653 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-971-217-103

Alignment Scores:
Pred. No.: 1,18e-27 Length: 653
Score: 261.00 Matches: 51
Percent Similarity: 62.50% Conservative: 24
Best Local Similarity: 42.50% Mismatches: 44
Query Match: 40.03% Indels: 1
DB: 2 Gaps: 0

US-10-005-429-14 (1-126) x US-08-971-217-103 (1-653)
Qy 2 AlaAlaGluGluGluValValIleAlaCysHisThrLysAspGluPheAspAlaArgMet 21
Db 69 TCATCCGAGGAGGACAAAGTGTTCGGCTGCCCAAGGTTGAGGAATGGAACGAGTACTTC 128
Qy 22 AlaLysAlaLysGluGlnGlyLysLeuValValIleAspPheMetAlaProTTPCySer 41
Db 129 AAGAAAGGCGTTGAGACTAAGAACTGGTGGTGGTTCGATTTTACTGCTTCATGTCGGGS 188
Qy 42 GlyCysGlnMetMetAlaProValTyAlaLysCysAlaSerLysTyrProSerAlaVal 61
Db 189 CCTTGGCGTTTATTGGCCCAATCTTGTGACATGCTAAGAAAGCCCATGTTTATA 248
Qy 62 PheLeuGluValAspValAspGluLeuLeuGluValAlaLysIleTyrGlyValHisVa 81

```

Db 249 TTCTCAAGGTGATGTTGATGAAGTGTTCAGCGGAGTGGAGGC 308
Qy 81 lMetProthrPheCysPheIleArgAsnGlyGluThrLeuGluSerPheAlaThrValas 101
Db 309 AATGCCAATTTTGTCTTCAATTAAGATGGAAGAGTGGACAGAGTTGTGTGCGCAA 368
Qy 101 pGluaspGluLeuArgAspAlaValaArgGlyTyraAlaAlaGlyThrThrAla 120
Db 369 GAAAGAGGAGTTCAGACAGACCATAGTGAAGCATGCTCTCTGCTACTGTCATGCT 426

RESULT 15
US-09-350-600-103
Sequence 103, Application US/09350600
Patent No. 6262342
GENERAL INFORMATION:
APPLICANT: Meins, Frederick
APPLICANT: Shinshi, Hideaki
APPLICANT: Wenzler, Herman
APPLICANT: Hofsteenge, Jan
APPLICANT: Ryals, John
APPLICANT: Sperisen, Christoph
TITLE OF INVENTION: DNA SEQUENCES ENCODING POLYPEPTIDES
TITLE OF INVENTION: HAVING BETA-1,3-GLUCANASE ACTIVITY
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6262342artis Corporation
STREET: 3054 Cornwallis Road, P.O. Box 12257
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/350,600
FILING DATE:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/971,217
FILING DATE: 14-NOV-1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/457,364
FILING DATE: 31-MAY-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/181,271
FILING DATE: 13-JAN-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT 1989

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/381,443
FILING DATE: 18-JUL-1989
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/353,312
FILING DATE: 17-MAY-1989
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/226,303
FILING DATE: 29-JUL-1988
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-198250
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 103:
SEQUENCE CHARACTERISTICS:
LENGTH: 653 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-350-600-103

Alignment Scores:
Pred. No.: 1.18e-27
Score: 261.00
Percent Similarity: 62.50%
Best Local Similarity: 42.50%
Query Match: 40.03%
DB: 3
Gaps: 0

US-10-005-429-14 (1-126) x US-09-350-600-103 (1-653)

Qy 2 AlalaGluGluGlyAlaValaIleAlaCysHisThrLysAspGluPheAspAlaArgMet 21
Db 69 TCATCCGAGGAGGACCAAGTGTTCGGCTGCCACCAAGTTGAGGATGGAACAGTACTTC 128
Qy 22 AlAlaLysAlaLysGluGlnGlyLysLeuValValIleAspPheMetAlaProTrpCysSer 41
Db 129 AAGAAAGCGCTTGAGACTAAGAACTGGTGTGTGCGATTCTGCTTCTATGCTGCGGS 188
Qy 42 GlyCysGlnMetAlaProValTyAlaAspCysAlaSerLysTyProSerAlaVal 61
Db 189 CTTTGGCGTTTATTGCCCCAAATCTTGTGACATTCCTAAGAAAGATGCCCATGTTATA 248
Qy 62 PheLeuGluValAspValAspGluLeuValAlaLysIleTyGlyValHisVa 81
Db 249 TTCTCAGGTTGATGTGATGAACTGAGACTGTTTCAGCGGGAATGAGTGTGGAGGC 308
Qy 81 lMetProthrPheCysPheIleArgAsnGlyGluThrLeuGluSerPheAlaThrValas 101
Db 309 AATGCCAATTTTGTCTTCAATTAAGATGGAAGAGTGGACAGAGTTGTGTGCGCAA 368

QY 101 pGluAspGluLeuArgAspAlaValArgLysTyrAlaAlaAlaGlyThrThrAla 120
Db 369 GAAAGAGGAGTTGCAGCAGACCATAGTGAAGCATGCTCTCTGCTACTGCTGCT 426

Search completed: May 5, 2004, 07:45:44
Job time : 50.3939 secs

US-10-425-114-16798

Alignment Scores:
 Pred. No.: 1,378-87 Length: 731
 Score: 652.00 Matches: 126
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 13 Gaps: 0

US-10-005-429-14 (1-126) x US-10-425-114-16798 (1-731)

Qy 1 MetAlaAlaGluGluGlyAlaValIleAlaCysHisThrLysAspGluPheAspAlaArg 20
 Db 49 ATGGCGCGCGAGAGAGTCCGCGTATCGCGTCCACACAGGAGAGTTCCACCGCCGC 108
 Qy 21 MetAlaLysAlaLysGluGlnGlyLysLeuValIleAspPheMetAlaProTyrCys 40
 Db 109 ATGGCCAAAGCCCAAGGAGCGAGGCAAGCTGGTGTATCGACTTCATGGCCCCCTGGTGC 168
 Qy 41 SerGlyCysGlnMetMetAlaProValTyrAlaAspCysAlaSerLysTyrProSerAla 60
 Db 169 AGTGGGTGCAGATGATGCGCCCGGTGTACGGGACTGCGCAGCAAGTACCTTTCCGCG 228
 Qy 61 ValPheLeuGluValAspValAspGluLeuValAlaLysIleTyrGlyValHis 80
 Db 229 GTCTTCCTCGAGGTTCAGCTCGACGACTGCTGGAGTGGCGAAGTCTACGGCGTCCAT 288
 Qy 81 ValMetProThrPheCysPheIleArgAsnGlyGluThrLeuGluSerPheAlaThrVal 100
 Db 289 GTGATGCGCGACCTTCGTTCATCAGGAACGGCGAGACGCTCGAGAGCTTTGCTACCGTC 348
 Qy 101 AspGluAspGluLeuArgAspAlaValArgLysTyrAlaAlaGlyThrThrAla 120
 Db 349 GACGAGGAGAGCTCCGGAGCGCGTCCAGAGTACCGCCGCTGGCACTACGACGCGCT 408
 Qy 121 ProAlaSerAlaSerAla 126
 Db 409 CTGCGCTCGCGGTCCGCC 426

RESULT 2

US-10-425-114-16904
 ; Sequence 16904, Application US/10425114
 ; Publication No. US20040034888A1

GENERAL INFORMATION:

APPLICANT: Liu, Jingdong
 APPLICANT: Zhou, Yihua
 APPLICANT: Kovalic, David K.
 APPLICANT: Screen, Steven E.
 APPLICANT: Tabaska, Jack E.
 APPLICANT: Cao, Yongwei
 TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 FILE REFERENCE: 38-21(5313)B
 CURRENT APPLICATION NUMBER: US/10/425,114
 CURRENT FILING DATE: 2003-04-28
 NUMBER OF SEQ ID NOS: 73128
 SEQ ID NO 16904
 LENGTH: 742
 TYPE: DNA
 ORGANISM: Zea mays
 FEATURE:
 OTHER INFORMATION: Clone ID: LIB3067-031-H6_FLI
 US-10-425-114-16904

Alignment Scores:
 Pred. No.: 1,48-87 Length: 742
 Score: 652.00 Matches: 126
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 13 Gaps: 0

US-10-005-429-14 (1-126) x US-10-425-114-16904 (1-742)

Qy 1 MetAlaAlaGluGluGlyAlaValIleAlaCysHisThrLysAspGluPheAspAlaArg 20
 Db 46 ATGGCGCGCGAGAGAGTCCGCGTATCGCGTCCACACAGGAGAGTTCCACCGCCGC 105
 Qy 21 MetAlaLysAlaLysGluGlnGlyLysLeuValIleAspPheMetAlaProTyrCys 40
 Db 106 ATGGCCAAAGCCCAAGGAGCGAGGCAAGCTGGTGTATCGACTTCATGGCCCCCTGGTGC 165
 Qy 41 SerGlyCysGlnMetMetAlaProValTyrAlaAspCysAlaSerLysTyrProSerAla 60
 Db 166 AGTGGGTGCAGATGATGCGCCCGGTGTACGGGACTGCGCAGCAAGTACCTTTCCGCG 225
 Qy 61 ValPheLeuGluValAspValAspGluLeuValAlaLysIleTyrGlyValHis 80
 Db 226 GTCTTCCTCGAGGTTCAGCTCGACGACTGCTGGAGTGGCGAAGTCTACGGGCTCCAT 285
 Qy 81 ValMetProThrPheCysPheIleArgAsnGlyGluThrLeuGluSerPheAlaThrVal 100
 Db 286 GTGATGCGCGACCTTCGTTCATCAGGAACGGCGAGACGCTCGAGAGCTTTGCTACCGTC 345
 Qy 101 AspGluAspGluLeuArgAspAlaValArgLysTyrAlaAlaGlyThrThrAla 120
 Db 346 GACGAGGAGAGCTCCGGAGCGCGTCCAGGAAGTACCGCCGCTGGCACTACGACGCGCT 405
 Qy 121 ProAlaSerAlaSerAla 126
 Db 406 CTGCGCTCGCGGTCCGCC 423

RESULT 3

US-10-425-114-17028
 ; Sequence 17028, Application US/10425114
 ; Publication No. US20040034888A1

GENERAL INFORMATION:

APPLICANT: Liu, Jingdong
 APPLICANT: Zhou, Yihua
 APPLICANT: Kovalic, David K.
 APPLICANT: Screen, Steven E.
 APPLICANT: Tabaska, Jack E.
 APPLICANT: Cao, Yongwei
 TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 FILE REFERENCE: 38-21(5313)B
 CURRENT APPLICATION NUMBER: US/10/425,114
 CURRENT FILING DATE: 2003-04-28
 NUMBER OF SEQ ID NOS: 73128
 SEQ ID NO 17028
 LENGTH: 752
 TYPE: DNA
 ORGANISM: Zea mays
 FEATURE:
 OTHER INFORMATION: Clone ID: LIB3067-048-H2_FLI
 US-10-425-114-17028

Alignment Scores:
 Pred. No.: 1,438-87 Length: 752
 Score: 652.00 Matches: 126
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 13 Gaps: 0

US-10-005-429-14 (1-126) x US-10-425-114-17028 (1-752)

Qy 1 MetAlaAlaGluGluGlyAlaValIleAlaCysHisThrLysAspGluPheAspAlaArg 20
 Db 56 ATGGCGCGCGAGAGAGTCCGCGTATCGCGTCCACACAGGAGAGTTCCACCGCCGC 115
 Qy 21 MetAlaLysAlaLysGluGlnGlyLysLeuValIleAspPheMetAlaProTyrCys 40
 Db 116 ATGGCCAAAGCCCAAGGAGCGAGGCAAGCTGGTGTATCGACTTCATGGCCCCCTGGTGC 175

QY 41 SerGlyCysGlnMetValProValTyrAlaAspCysAlaSerIysTyrProSerAla 60
 DB 176 AGTGGTGCAGATGATGGCCCGGTGTACGGACTCGCCAGCAAGTACCTTCGCG 235
 QY 61 ValPheLeuGluValAspValAspGluLeuGluValAlaValIleTyrGlyValHis 80
 DB 236 GTCTTCTCGAGTGCAGCTCGACGACTGCTGGAGTCCGAGATCTACGGCTCCAT 295
 QY 81 ValMetProThrPheCysPheIleArgAsnGlyGluThrLeuGluSerPheAlaThrVal 100
 DB 296 GTGATGCCGACCTTCTGCTTTCATCAGGACGGGAGAGCGCTCGAGAGCTTTGCTACCGTC 355
 QY 101 AspGluAspGluLeuArgAspAlaValArgLysTyrAlaAlaGlyThrThrAla 120
 DB 356 GACGAGACGAGCTCCGGACGCGTCAGGAAGTACGCCCGCCCTGGCACTACAGGCT 415
 QY 121 ProAlaSerAlaSerAla 126
 DB 416 CCTGCTCGCGCTCGGCC 433

RESULT 4

US-10-425-114-7100
 ; Sequence 7100, Application US/10425114
 ; Publication No. US2004003488A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Liu, Jingdong
 ; APPLICANT: Zhou Yihua
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Screen, Steven E
 ; APPLICANT: Tabaska, Jack E
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53313)B
 ; CURRENT APPLICATION NUMBER: US/10/425,114
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 73128
 ; SEQ ID NO 7100
 ; LENGTH: 780
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: 700617241_FLI
 ; US-10-425-114-7100

Alignment Scores:
 Pred. No.: 1,07e-84 Length: 780
 Score: 533.00 Matches: 124
 Percent Similarity: 98.44% Conservative: 2
 Best Local Similarity: 96.88% Mismatches: 0
 Query Match: 97.09% Indels: 2
 DB: 13 Gaps: 1

US-10-005-429-14 (1-126) x US-10-425-114-7100 (1-780)

QY 1 MetAlaAlaGluGluGlyAlaValIleAlaCysHisThrLysAspGluPheAspAlaArg 20
 DB 102 ATGGCGCCGAGGAGGTGCGGTGATCGCGTGCACACCAAGGACGAGTTGACGCCCGC 161
 QY 21 MetAlaLysAlaLysGluGlnGlyLysLeuValValIleAspPheMetAlaProTyrCys 40
 DB 162 ATGGCCAGGCCAGGAGGAGGCAAGCTGTGTGTATCGACTTCATGGCCCCCTCGTGC 221
 QY 41 SerGlyCysGlnMetMetAlaProValTyrAlaAspCysAlaSerIysTyrProSerAla 60
 DB 222 AGTGGGTGCCAGATGATGGCCCGCGGTGATCGCGACTGCGCCAGCAAGTACCTTCGCG 281
 QY 61 ValPheLeuGluValAspValAspGluLeuGluValAlaValIleTyrGlyValHis 80
 DB 282 GTCTTCTCGAGTGCAGCTCGACGAACTGCTGGAGTCCGAGATCTACGGCTCCAT 341
 QY 81 ValMetProThrPheCysPheIleArgAsnGlyGluThrLeuGluSerPheAlaThrVal 100

DB 342 GTGATGCCGACCTTCTGCTTTCATCAGGAACGGGAGAGCGCTCGAGAGCTTGTACCGTC 401
 QY 101 AspGluAspGluLeuArgAspAlaValArgLysTyr-----AlaAlaGlyThrThr 118
 DB 402 GACGAGACGAGCTCGGAACCGCTCAGGAAGTACCGCGCGCCGCCGCGCACTACG 461
 QY 119 ThrAlaProAlaSerAlaSerAla 126
 DB 462 ACGGCTCTCTGCTCGGCGTCCGCC 485
 RESULT 5
 US-10-349-782-12
 ; Sequence 12, Application US/10349782
 ; Publication No. US2003014361A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Yves Hatzfeld
 ; APPLICANT: Valerie Marie-No. US2003014361A1lle Frankard
 ; APPLICANT: Anne-Marie Droual
 ; TITLE OF INVENTION: Method for easy cloning and selection of chimeric DNA molecules
 ; FILE REFERENCE: 1187-15
 ; CURRENT APPLICATION NUMBER: US/10/349,782
 ; CURRENT FILING DATE: 2003-01-23
 ; PRIOR APPLICATION NUMBER: EP 02075373.7
 ; PRIOR FILING DATE: 2002-01-23
 ; NUMBER OF SEQ ID NOS: 12
 ; SOFTWARE: Patent in version 3.1
 ; SEQ ID NO 12
 ; LENGTH: 540
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Modified thioredoxin of Oryza sativa in vector pDONR201
 ; US-10-349-782-12

Alignment Scores:
 Pred. No.: 3.72e-44 Length: 540
 Score: 361.00 Matches: 70
 Percent Similarity: 71.77% Conservative: 19
 Best Local Similarity: 56.45% Mismatches: 33
 Query Match: 55.37% Indels: 2
 DB: 15 Gaps: 1

US-10-005-429-14 (1-126) x US-10-349-782-12 (1-540)

QY 1 MetAlaAlaGluGluGlyAlaValIleAlaCysHisThrLysAspGluPheAspAlaArg 20
 DB 58 ATGGCGCCGAGGAGGTGCGGTGATCGCTGCCACACAGGACGAGTTGACGCCCGCAG 117
 QY 21 MetAlaLysAlaLysGluGlnGlyLysLeuValValIleAspPheMetAlaProTyrCys 40
 DB 118 ATGACCAAGGCCAGGAGGCCCGGCAAGTGGTCATANTGACTTCACTGCTTCTCGTGC 177
 QY 41 SerGlyCysGlnMetMetAlaProValTyrAlaAspCysAlaSerIysTyrProSerAla 60
 DB 178 GGACCGTGCCTTCATCGCCCGCGGTGCTGCTGAATACGCCCAAAAGTTCCCTGGTCT 237
 QY 61 ValPheLeuGluValAspValAspGluLeuGluValAlaValIleTyrGlyValHis 80
 DB 238 GTCTTCTCGAGGTGATGTTGATGAGCTGAAGGAGTTGCTGAAAGATACATGTGCGAG 297
 QY 81 ValMetProThrPheCysPheIleArgAsnGlyGluThrLeuGluSerPheAlaThrVal 100
 DB 298 GCATGCGCCAGCTTCTCTATTTCATCAGGATGTGTGCTGAGGCTGCAAGGTCTGTGGCGCC 357
 QY 101 AspGluAspGluLeuArgAspAlaValArgLysTyrAlaAlaGlyThrThrAla 120
 DB 358 AGGAGGATGAGCTCCAGAACCATCGTGAAGCAC-----GTCGTCGCCACTGCTGCA 411
 QY 121 ProAlaSerAla 124
 DB 412 TCTGCTTCTGCC 423

RESULT 6

```
US-10-425-114-26038
; Sequence 26038, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 26038
; LENGTH: 684
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB4073-004-E6_FLI
US-10-425-114-26038
Alignment Scores:
Pred. No.: 3.5e-43 Length: 684
Score: 355.50 Matches: 72
Percent Similarity: 69.70% Conservative: 20
Best Local Similarity: 54.55% Mismatches: 33
Query Match: 54.52% Indels: 7
DB: 13 Gaps: 1
US-10-005-429-14 (1-126) x US-10-425-114-26038 (1-684)
QY 1 MetAlaAlaGluGluGlyAlaValIleAlaCysHisThrLysAspGluPheAspAlaArg 20
DB 93 ATGGGTCTCGAGGAGGGAGTCTGTCATCGCTGCCACCAAGCGCGAGTTGACGCCCGAG 152
QY 21 MetAlaLysAlaLysGluGlnGlyLysLeuValIleAspPheMetAlaProTrpCys 40
DB 153 ATGGCAAGCCAGAGAGCGCGGAGCTGTGTGTTGATTTGATTTGATTTGATTTGATTTG 212
QY 41 SerGlyCysGlnMetMetAlaProValTyrrAlaAspCysAlaSerIlystYrProSerAla 50
DB 213 GGTCTTGGCGGCCATCGCTCCACTGTTGTGAGCAGCCCAAGAGTACACTCAAGCT 272
QY 61 ValPheLeuGluValAspValAspGluLeuLeuGluValAlaLysIleTyrrGlyValHis 80
DB 273 GTCTTCTCGAGGTGACGTGACGAACTGAAGGAGTTACTGCAGAGTACAGATCGAG 332
QY 81 ValMetProThrPheCysPheIleArgAsnGlyGluThrLeuGluSerPheAlaThrVal 100
DB 333 GCGATCCGACCTTCCACTTCATCAAGAACGGGAGCGGTGAGACTATCGTGGTGCC 392
QY 101 AspGluAspGluLeuArgAspAlaValArgLysTyrrAlaAlaGly----- 116
DB 393 AGGAAGGACGAGCTCTCGCCCTGTGATCCAGAGCATACCGCGTCTCGCTCCGCGTAAGAA 452
QY 117 -----ThrThrAlaProAlaSerAlaSer 125
DB 453 GATAGTCAGTCGTCTGTCATATAGGGCCAGCGCATCG 488
RESULT 7
US-10-425-114-23491
; Sequence 23491, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 23491
; LENGTH: 596
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3596-054-E10_FLI
US-10-425-114-23491
Alignment Scores:
Pred. No.: 3.02e-41 Length: 596
Score: 342.00 Matches: 65
Percent Similarity: 70.00% Conservative: 19
Best Local Similarity: 54.17% Mismatches: 36
Query Match: 52.45% Indels: 0
DB: 13 Gaps: 0
US-10-005-429-14 (1-126) x US-10-425-114-23491 (1-596)
QY 1 MetAlaAlaGluGluGlyAlaValIleAlaCysHisThrLysAspGluPheAspAlaArg 20
DB 65 ATGGGTCTCGAGGAGGGAGTCTGTCATCGCTGCCACCAAGCGCGAGTTGACGCCCGAC 124
QY 21 MetAlaLysAlaLysGluGlnGlyLysLeuValIleAspPheMetAlaProTrpCys 40
DB 125 ATGCCCAAGGCCAAGGAGCGCGGCAAGCTGTGTGATTCATTGACTTCAACGCTCTCTGTGC 184
QY 41 SerGlyCysGlnMetMetAlaProValTyrrAlaAspCysAlaSerLysTyrrProSerAla 60
DB 185 GGCCCTTCCGCTTCATCGCGCACTGTCTGTCGAGCAGCCCAAGAGTTCAACCCAGGCT 244
QY 61 ValPheLeuGluValAspValAspGluLeuLeuGluValAlaLysIleTyrrGlyValHis 80
DB 245 GTGTTCTCTGAAGGTGAGCGTGTGACGAGCTGAAGGAGTTGCCGCGCTCTACATGTCGAG 304
QY 81 ValMetProThrPheCysPheIleArgAsnGlyGluThrLeuGluSerPheAlaThrVal 100
DB 305 GCGATCCGACCTTCCACTTCGTCAAGAACGGGTGACGGTGGAGACCGTCTCGGTGCC 364
QY 101 AspGluAspGluLeuArgAspAlaValArgLysTyrrAlaAlaGlyThrThrAla 120
DB 365 AGGAAGGAGAACCTCTCTGCGCCCGAGATCGAAGAGCACTCGCGCGCGCGTCTGTCTGTCG 424
RESULT 8
US-10-425-114-23500
; Sequence 23500, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 23500
; LENGTH: 548
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3596-057-G4_FLI
US-10-425-114-23500
```


Db	176	GGTCCATGCGCGCCATGCCCCACTGTTCTGTCGACACGCCAAGAGATTCACTCAGGTC	235
Qy	61	ValPheLeuGluValAspValAspGluLeuGluValAlaLysIleTyrGlyValHis	80
Db	236	GTCTTCTGAAGTGGAAGTGAAGTGAAGGAGTCAACGGGCTACGAGGTCGAG	295
Qy	81	ValMetProThrPheCysPheIleArgSndGlyGlnThrLeuGluSerPheAlaThrVal	100
Db	296	GGATCCGACCTTCACCTTCGTCAAGAACGGCAAGACGGTGCACCATCGTGGGTGCC	355
Qy	101	AspGluAspGluLeuArgAspAlaValArgLysTyrAlaAlaGlyThrThrAla	120
Db	356	AGAAGGAGAGACTCTGTGGCCCTGATCGAAGAGCATGCGCG	403
Qy	121	ProAlaSerAlaSerAla	126
Db	404	CCTGGCTGTGGCTGTGCC	421

RESULT 11
US-10-260-238-5754

Alignment Scores:		
Pred. No.:	5,92e-41	366
Score:	338.00	67
Percent Similarity:	69.05%	20
Best Local Similarity:	53.17%	35
Query Match:	51.84%	4
DB:	16	1
		Gaps:
		Indels:
		Mismatches:
		Conservative:
		Matches:
		Length:

US-10-005-429-14 (1-126) x US-10-260-238-5754 (1-366)

Qy		1	MetalAlaGluGluGlyValValIleAlaCysHisThrLysAspGluPheAspAlaArg	20
Dd		1	ATGGCGTCCAGACGGAGTGCTGATCGTCGCCACAGCAAGCTGAGTTGCAGCCGCAC	60
Qy		21	MetalLysAlaLysGluGlnGlyLysLeuValValIleaspPheMetAlap-ofrPcys	40
Dd		61	ATGACCAAGGCCACAGAAACCGCAAGCTGTGTGTCATCGACTTCATGCGCGCTGTGC	120
Qy		41	SerGlyCysGlnMetMetalProValTyrrAlaaspCysAlaserLysTyrrProSerAla	60
Dd		121	GSTCATCCCGCGGCATCGCCCCCATCTGTGTGCACACGCCAAGAAGTTCATCTCAGGTC	180

Qy	61	ValPheLeuGluValAspValAspGluLeuLeuGluValAlaLysIleTyrGlyValHis	80
		:::	
		:::	
Db	181	GTCTTCCTGAGGTGCAGCTGACGAAGTGAAGAGTACCCTGCGCTACGAGGTCGAG	240
Qy	81	ValMetProThrPheCysPheIleArgAsnGlyGluThrLeuGluSerPheAlaThrVal	100
		:::	
		:::	
Db	241	GGCATGCCGACCTTCCATCTCTGACAAACGGCAGACGGTCGGACCATCGTGGGTGCC	300
Qy	101	AspGluAspGluLeuArgAspAlaValArgIlystTyrAlaAlaAlaGlyThrThrThrAla	120
		:::	
Db	301	AGGAGGACGAGCTCTCTGCCACATCGAGAGCATGCCGG-----CCTGGC	348
Qy	121	ProIleSerAlaSerAla	126
Db	349	CCTGGCTCTGGCTCTGCC	366

RESULT 12
US-10-425-114-35628

	Alignment Scores:		Length:
Pred. No.:	1,119-40	Matches:	565
Score:	338.00	Conservative:	67
Percent Similarity:	69.0%	Mismatches:	20
Best Local Similarity:	53.1%	Gaps:	35
Query Match:	51.8%	Indels:	4
DB:	13		1

US-10-005-429-14 (1-126) X US-10-425-114-35628 (1-565)

Qy	1	MetAlaAlaGluGluGluValAlaValAlaCysHisThrLysAspGluPheAspAlaArg	20
Db	35	ATGGCGCTCCGAGCGAGTGTGTATCGCTGCCACCAAGCGCTGAGTTTCGACGCCAC	94
Qy	21	MetAlaLysAlaLysGluGluGlnGlyLysLeuValValLeuAspPheMetAlaProTyrCys	40
Db	95	ATGACCAAGGCCAGGAAGCCGCAAGCTGGTGTCTATCGACTTCACTGCCGCGCTGGTGC	154
Qy	41	SerGlyCysGlnMetMetAlaProValTyrAlaAspCysAlaSerLysTyrProSerAla	60
Db	155	GCTCATTCGCGGCGCATTCGCCCCACTGTTCTGTGCACACGCCAAGAGTTCACTCAGGTC	214
Qy	61	ValPheLeuGluValAspValAspGluLeuGluValAlaLysIleTyrGlyValHis	80
Db	215	GTCTTCTTGAAGGTGGACGTGCAGCAAGTGAAGAAAGTCAACCGCGCTACAGAGTTCGAG	274
Qy	81	ValMetProThrPheCysPheIleArgAsnGlyGluThrLeuGluSerPheAlaThrVal	100
Db	275	GGATGCGCGACCTTCCACTTCGTCAAGAAAGCGCAAGACGTCGCGACCATCGTGGGTGGCC	334
Qy	101	AspGluAspGluLeuAlaGAspAlaValArgLysTyrAlaAlaGlyThrThrAla	120

Db	335	AGGAGAGGAGAGCTCCTGGCCAGATCGAAGCATGCCGCG-----CCTGGCG	382
Qy	121	ProAlaSerAlaSerAla	126
Db	383	CCTGGCTGTGGCTTGCC	400

RESULT 13

```

US-10-425-114-284
: Sequence 284, Application US/10425114
: Publication NO. US20040034888A1
: GENERAL INFORMATION:
: APPLICANT: Liu, Jingdong
: APPLICANT: Zhou, Yihua
: APPLICANT: Kovalic, David K.
: APPLICANT: Screen, Steven E.
: APPLICANT: Tabaska, Jack E.
: APPLICANT: Cao, Yongwei
: TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
: TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
: FILE REFERENCE: 38-2153313/B
: CURRENT APPLICATION NUMBER: US/10/425,114
: CURRENT FILING DATE: 2003-04-28
: NUMBER OF SEQ ID NOS: 73128
: SEQ ID NO 284
: LENGTH: 583
: TYPE: DNA
: ORGANISM: Zea mays
: FEATURE:
: OTHER INFORMATION: Clone ID: 700052149_FLI
US-10-425-114-284

```

Alignment Scores:	
Pred. No.:	1.16e-40
Score:	338.00
Percent Similarity:	69.05%
Best Local Similarity:	53.17%
Query Match:	1.84%
DB:	13
	Gaps: 1
	Indels: 4
	Mismatches: 35
	Conservative: 20
	Matches: 67
	Length: 583

US-10-005-429-14 (1-126) x US-10-425-114-284 (1-583)

[illegible]

167 GGTCCATCCGGCGCCATCCGCCCACTGTTGTCGACACGCCAAGAGGTTCTACTCAGTCC 226
Db Db
61 ValPheLeuGluValAspValAspGluLeuLeuGluValAlaLysIleTyrGlyValHis 80
Oy Oy
227 GTCTTCCGAAAGGTGGACGTGGACGAATCAAGAGATCCACGCCCTACAGAGTCCAG 286
Db Db
81 ValMetProThrPheCysPheIleArgAsnGlyGluThrLeuGluSerPheAlaThrVal 100
Oy Oy

287	CGGATGCCGACCTTCACATTCGTCTCAAGACGGCAGACGTCGCGACCATCTGGTGGCC	346
Db		
101	AspGluAspGluLeuArgAspAlaValArgLysTyrAlaAlaGlyThrThrThrAla	120
Qy	::: :::::	
347	AGGAAGACGAGCTCTGGGCCAGATCGAAGACATGCCGCG	394
Db		
121	ProAlaSerAlaSerAla	126
Qy		

Db 395 CCTGGCTGGCTGGC 412
 RESULT 14
 US-10-425-114-17618
 ; Sequence 17618, Application US/10425114
 ; Publication No. US20040034889A1

; GENERAL INFORMATION:
 ; APPLICANT: Liu, Jingdong
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Koralic, David K.
 ; APPLICANT: Screen, Steven E.
 ; APPLICANT: Tabaska, Jack B.
 ; APPLICANT: Cao, Yongwei

US-10-425

```

? TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
?
? TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
?
? FILE REFERENCE: 38-21(53313)B
?
? CURRENT APPLICATION NUMBER: US/10/425,114
?
? CURRENT FILING DATE: 2003-04-28
?
? NUMBER OF SEQ ID NOS: 73128
?
? SEQ ID NO 17618
?
? LENGTH: 594
?
? TYPE: DNA
?
? ORGANISM: Zea mays
?
? FEATURE:
?
? OTHER INFORMATION: Clone ID: LIB3070-001-G9_FLI
?
? US-10-425-114-17618

```

Alignment Scores:	
Pred. No.:	1.2e-40
Score:	338.00
Percent Similarity:	69.05%
Best Local Similarity:	53.17%
Query Match:	51.94%
DB:	13
Gaps:	1
Indels:	4
Mismatches:	35
Conservative:	20
Matches:	67
Length:	594

US-10-005-429-14 (1-126) x US-10-425-114-17618 (1-594)

1 MetAlaLaGluGluGlyAlaValIleAlaCysHisThrLysAspGluPheAspAlaArg 20
58 ATGCGTCGTCAGCAGGAGCGCGTATCGCGTCCACAGCAAGCGCTAGTTCGACGCCAC 117
21 MetAlaLysAlaLysGluGlnGlyLysLeuValIleAspPheValAlaProTrpCys 40
118 ATGACCAAGCCGACAGAGCCGCAAGCTGGTGGTTCATCGATTCACTCGCCCTGGTGC 177

41 SerGlyCysGlnMetMetAlaProValTyrAlaAspCysAlaSerLysTyrProSerAla 60

178	GGTCCATGCGCGCCCATCGCCCATGTTCTGCGAAACGCCAAGAGTTCTACTCAGTCC	237
61	ValPheLeuGluValAspValAspGluLeuLeuGluValAlaLysIleTyrGlyValHis	80
238	GTCTCTCGAAGGTGACGTGGACGAAGTGAAGGAAGTACCGCGCGCTACAGAGTCGAG	297
81	ValMetProThrPheCysPheIleArgAsnGlyGluThrLeuGluSerPheAlaThrVal	100
298	GGCATGGCGACCTTCATCTCGTCAAGAACCGCAAGACGGTCGGACCATATGGTGTCGC	357

101 AspCluAspCluLeuArgAspAlaValArgIysTyrAlaAlaGlyThrThrAla 120
 :::|:::|:::|:::|:::|:::|
358 AGAAGGACGAGCTCTGTGCCGATCGAGAAGCATGCCGG-----CCTCCG 405

121 ProAlaserAlaserAla 126
 |||
406 CCTGCCTTCGGTCTGCC 423
DB

RESULT 15
US-10-425-114-23337
; Sequence 23337, Application US/10425114
; PublicationNo. US20040034888A1

GENERAL INFORMATION:

APPLICANT: Liu, Jingdong
 APPLICANT: Zhou Yihua
 APPLICANT: Kovalic, David K.
 APPLICANT: Screen, Steven E
 APPLICANT: Tabaska, Jack E
 APPLICANT: Cao, Yongwei
 TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 FILE REFERENCE: 38-21 (531)3R

; CURRENT APPLICATION NUMBER: US/10/425,114
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 73128
 ; SEQ ID NO 23337
 ; LENGTH: 692
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: LIB3595-039-B9_FLI
 US-10-425-114-23337

Alignment Scores:
 Pred. No.: 1,498-40 Length: 692
 Score: 338.00 Matches: 67
 Percent Similarity: 69.05% Conservative: 20
 Best Local Similarity: 53.17% Mismatches: 35
 Query Match: 51.84% Indels: 4
 DB: 13 Gaps: 1

US-10-005-429-14 (1-126) x US-10-425-114-23337 (1-692)

Qy	1	MetAlaAlaGluGluGlyAlaValIleAlaCysHisThrLysAspGluPheAspAlaArg	20
Db	16	ATGGCGTCGAGCAGGAGTCTGATCGCGTGCCACAGCAAGGCTGAGTTGACGCCAC	75
Qy	21	MetAlaLysAlaLysGluGlnGlyLysLeuValIleAspPheMetAlaProTyrCys	40
Db	76	ATGACCAAGGCCAGGAAGCCGCGAAGCTGGTGGTCACTGACTTCACTGCCCGCTGGTGC	135
Qy	41	SerGlyCysGlnMetMetAlaProValTyrAlaAspCysAlaSerIleTyrProSerAla	60
Db	136	GTCCATGCGCGCCATCGCCCTCTGTCGAAACACGCCAAGAGTTCACCTCAGGTC	195
Qy	61	ValPheLeuGluValAspValAspGluLeuLeuValAlaLysIleTyrGlyValHis	80
Db	196	GTCTTCCTGAGGTGGAGTGGACGAGTGAAGGAAGTACCGCGGCTACGAGTGGAG	255
Qy	81	ValMetProThrPheCysPheIleArgAsnGlyGluThrLeuGluSerPheAlaThrVal	100
Db	256	GGATGCGGACCTTCCACTTCTCAAGACCGCAAGACGGTCGCGACCATCGTGGTGCC	315
Qy	101	AspGluAspGluLeuArgAspAlaValArgLysTyrAlaAlaAlaGlyThrThrAla	120
Db	316	AGGAAGGACGAGTCTCTGGCCCGACGATCGAGAAGCATGCCGCG-----CCTGCG	363
Qy	121	ProAlaSerAlaSerAla	126
Db	364	CTGCGTCTGCGTCTGCC	381

Search completed: May 5, 2004, 08:36:29
 Job time: 184.319 secs

207 LysileLysValLeuTrpAspSerGluValValGluAlaValGlyAlaAsnGlyGly 226
 625 AAGATTGATGTTGGAACCTCTCTGTTGGAAGCTTATGAGAGATGAGAGAT 694
 227 ProLeuAlaGlyValLysValLysAsnLeuAsnGlyGluValSerAspLeuGlnVal 246
 685 GTGCTTGGAGATTGAAGTGAAGATGTGTACCGAGATGTTCTGATTTAAAGTT 744
 247 SerGlyLeuPheAlaIleGlyHisGluProAlaThrLysPheLeuGlyGlnLeu 266
 745 TCTGGATTGTTCTTGTCTATGTTGTCATGAGCCAGCTACCAAGTTTGTGGTGTGT 804
 267 GluLeuAspSerAspGlyValGluThrLysProGlySerThrHisThrSerValLys 286
 805 GAGTTAGATTGGAGTGTATGTTGTCAGAGCTGTGTTACTTACACAGATAGCTTCCC 864
 287 GlyValPheAlaAlaGlyAspValGlnAspLysValGlnAlaIleThrAlaAla 306
 865 GGAGTTTTCGCTGCGGTGATGTTTCAGGATAAGAGTATAGGCAAGCATCACTGTGCA 924
 307 GlySerGlyCysMetAlaAlaLeuAspAlaGluHisTyrLeuGlnGluIleGlyAlaGln 326
 925 GGAACCTGGTGCATGGCAGCTTGGATGCGAGCATTTACTTACAGAGATTGGATCTCAG 984
 327 GluGlyLysSerAsp 331
 985 CAAGGTAAAGATGAT 999

RESULT 15
 US-10-290-072-238
 ; Sequence 238, Application US/10290072
 ; Publication No. US20030211511A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Briggs, Steven P.
 ; APPLICANT: Daima, Bipin K.
 ; APPLICANT: del Val, Greg
 ; APPLICANT: Desjarlais, John R.
 ; APPLICANT: Heifetz, Peter
 ; APPLICANT: Luginbuhl, Peter
 ; APPLICANT: Muchhal, Umesh
 ; TITLE OF INVENTION: Nucleic Acids and Proteins with Thioredoxin Reductase Activity
 ; FILE REFERENCE: A-71457-3
 ; CURRENT APPLICATION NUMBER: US/10/290,072
 ; CURRENT FILING DATE: 2002-11-06
 ; PRIOR APPLICATION NUMBER: US 60/370,609
 ; PRIOR FILING DATE: 2002-04-05
 ; PRIOR APPLICATION NUMBER: US 60/376,682
 ; PRIOR FILING DATE: 2002-04-29
 ; PRIOR APPLICATION NUMBER: US 10/141,531
 ; PRIOR FILING DATE: 2002-05-06
 ; PRIOR APPLICATION NUMBER: US 60/285,029
 ; PRIOR FILING DATE: 2001-05-04
 ; NUMBER OF SEQ ID NOS: 239
 ; SOFTWARE: Patent version 3.2
 ; SEQ ID NO 238
 ; LENGTH: 1344
 ; TYPE: DNA
 ; ORGANISM: Artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: synthetic
 US-10-290-072-238

Alignment Scores:
 Pred. No.: 7,79e-160 Length: 1344
 Score: 1318.00 Matches: 254
 Percent Similarity: 86.77% Conservative: 28
 Best Local Similarity: 78.15% Mismatches: 39
 Query Match: 77.12% Indels: 4
 DB: 13 Gaps: 1

11 ThrArgIleCysIleIleGlySerGlyProAlaAlaHisThrAlaAlaIleThrAlaAla 30
 367 ACAGGCTCTGATGTTAGAGAGTGGCCGCGGACACACACGCGGCGGATTTACGCGACT 426
 31 ArgAlaGluLeuLysProValLeuPheGluGlyTrpMetAlaAsnAspIleAlaAlaGly 50
 427 AGGCTGAACTTAAACCTCTCTTCGAAGGATGGATCGCTAAACGACATCGCTCCCGGT 486
 51 GlyGlnLeuThrThrThrThrAspValGluAsnPheProGlyPheProAsnGlyIleMet 70
 487 GGTCAACTAACACACACACCGAGCTCGAGATTTCCCGGATTTCCAGAGGATTTCTC 546
 71 GlyAlaAspLeuMetAspAsnCysArgAlaGlnSerLeuArgPheGlyThrAsnIleLeu 90
 547 GAGTAGAGCTCCTGACAAATTCGTAACCAATCGAGCGATTCGGTACTACGATATTT 606
 91 SerGluThrValThrAlaValAspPheSerAlaCysProPheArgValSerAlaAspSer 110
 607 ACAGAGCGGTGACGAAAGTCTGATTTCTCTCGAACCCGTTTAAAGCTATTCACAGATTCA 666
 111 ThrThrValLeuAlaAlaAlaValIleValAlaThrGlyAlaValAlaAlaArgArgLeuHis 130
 667 AAAGCCATTCTCGCTGAGCTGTGATTTCTCGCTACTGAGCTGTGGCTAAGCGCTTAGC 726
 131 Phe-----ProGlySerAspAlaTyrTrpAsnArgGlyIleSerAlaCysAla 146
 727 TCGTTGGATCTGGTGAAGGTTCTGGAACCGTGAATCTCCGCTTGTGCT 786
 147 ValCysAspGlyAlaAlaProIlePheArgAsnLysProIleAlaValIleGlyGlyGly 166
 787 GTTTGCGAGGAGCTCTCGATATTCGGTAAACAACTCTTGGCTGATCGGTGGAGGC 846
 167 AspSerAlaMetGluSerAsnPheLeuThrLysTyrGlySerHisValTyrIleIle 186
 847 GATTGCAATGGAAGACAACTTCTTACAAAATATGGATCTTAAAGTGTATATAATC 906
 187 HisArgAsnThrPheArgAlaSerLysIleMetGlnAlaAlaArgAlaLeuGluAsnPro 206
 907 CATAGGAGATGCTTTTGAAGCTTGAAGATTTATGACAGCGAGCTTGTCTAATCCT 966
 207 LysileLysValLeuTrpAspSerGluValValGluAlaTyrGlyAlaAsnGlyGly 226
 967 AAGATTGATGTTGGAACCTCTCTGTTGTTGGAAGCTTATGAGATGGAAGAGAT 1026
 227 ProLeuAlaGlyValLysValLysAsnLeuLeuAsnGlyGluValSerAspLeuGlnVal 246
 1027 GTGCTTGGAGATTGAAGTGAAGATGTTGTTACCGGAGATGTTTCTGATTTAAAGTT 1086
 247 SerGlyLeuPheAlaIleGlyHisGluProAlaThrLysPheLeuGlyGlnLeu 266
 1087 TCTGGATTGTTCTTGTCTATGTTGTCATGAGCCAGCTACCAAGTTTGTGGATGTTGT 1146
 267 GluLeuAspSerAspGlyValGluThrLysProGlySerThrHisThrSerValLys 286
 1147 GAGTTAGATTGGATGTTATGTTGTCAGAGCTGTGTTACTTACAGAGATAGCTTCCC 1206
 287 GlyValPheAlaAlaGlyAspValGlnAspLysValGlnAlaIleThrAlaAla 306
 1207 GAGATTTCGCTGCGGTGATGTTTCAGGATAAGAGTATAGGCAAGCATCACTGTGCA 1266
 307 GlySerGlyCysMetAlaAlaLeuAspAlaGluHisTyrLeuGlnGluIleGlyAlaGln 326
 1267 GGAACCTGGTGCATGGCAGCTTGGATGCGAGCATTTACTTACAGAGATTGGATCTCAG 1326
 327 GluGlyLysSerAsp 331
 1327 CAAGGTAAAGATGAT 1341

Search completed: May 5, 2004, 08:36:40
 Job time : 463.681 secs

```
Db 25 ACAAGCTCTGTATAGAGTGGCCAGCGCCACACACGCGGCGATTACGCGCT 84
Qy 31 ArgAlaGluLeuLysProValLeuPheGluGlyTrpMetAlaAsnAspIleAlaGly 50
Db 85 AGGGCTGAACCTTAACCTCTCTCTCGAAGGATGGATGCTAACGACATCGCTCCGGT 144
Qy 51 GlyGlnLeuThrThrThrAspValGluAsnPheProGlyPheProAsnGlyIleMet 70
Db 145 GGTCACTAACACACCGAGCTGAGAAATTCCTCCGGAATTCCTCCAGAGGTATTC 204
Qy 71 GlyAlaAspLeuMetAspAsnCysArgAlaGlnSerLeuArgPheGlyThrAsnIleLeu 90
Db 205 GCGATGAGCTCACTGACCAATTCCTGTAACAAATCGAGCGATTCGGTACTACGATATT 264
Qy 91 SerGluThrValThrAlaValAspPheSerAlaCysProPheArgValSerAlaAspSer 110
Db 265 ACAGAGCGGTGACGAAAGTCGATTCCTTCGAAACCGTTTAAGCTATTCACAGATTCA 324
Qy 111 ThrThrValLeuAlaAspAlaValIleValAlaThrGlyAlaValAlaArgLeuHis 130
Db 325 AAAGCCATTCCTCGCTGACGCTGTGATTCCTGCTACTGAGCTGTGGCTAGCGCTTAGC 384
Qy 131 Phe-----ProGlySerAspAlaTyTrpAsnArgGlyIleSerAlaCysAla 146
Db 385 TTCGTTGGATCTGGTGAAGGTTCTGGAGGTTCTCGAACCGTGAATCTCCGCTTGCT 444
Qy 147 ValCysAspGlyAlaAlaProIlePheArgAsnLysProIleAlaValIleGlyGly 166
Db 445 GTTTCGCGAGGAGCTGCTCCGATATTCGTAACAACTCTTCGCGGTATCGGTGAGGC 504
Qy 167 AspSerAlaMetGluGluSerAsnPheLeuThrLysTyTrpGlySerHisValTrpIle 186
Db 505 GATTGAGCAATCGAAGAACAACTTCTTCAAAATATGGATCTAAAGTGATATATTC 564
Qy 187 HisArgArgAsnThrPheArgAlaSerLysIleMetGlnAlaArgAlaLeuGluAsnPro 206
Db 565 CATAGGAGATGCTTTTAGACGCTTAAGATTAATGACGACGCGAGCTTTGTCTAATCT 624
```

RESULT 14

US-10-032-201B-10

; Sequence 10, Application US/10032201B

; Publication No. US20030167524A1

; GENERAL INFORMATION:

; APPLICANT: Van Rooijen, Gijb

```
; APPLICANT: Deckers, Harm
; APPLICANT: Heifetz, Peter Bernard
; APPLICANT: Briggs, Steven
; APPLICANT: Dalmia, Bipin Kumar
; APPLICANT: Del Val, Greg
; APPLICANT: Zaplachinski, Steve
; APPLICANT: Moloney, Maurice
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED
; FILE REFERENCE: 38814 351B
; CURRENT APPLICATION NUMBER: US/10/032, 201B
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 313
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 1002
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1002)
; OTHER INFORMATION: cDNA encoding NADPH thioresdoxin reductase
US-10-032-201B-10
```

```
Alignment Scores:
Pred. No.: 5,01e-160 Length: 1002
Score: 1318.00 Matches: 254
Percent Similarity: 85.77% Conservative: 28
Best Local Similarity: 78.15% Mismatches: 39
Query Match: 77.12% Indels: 4
DB: 15 Gaps: 1
```

US-10-005-429-25 (1-331) x US-10-032-201B-10 (1-1002)

```
Qy 11 ThrArgIleCysIleIleGlySerGlyProAlaAlaHisThrAlaAlaIleTyrAlaAla 30
Db 25 ACAAGCTCTGTATAGAGTGGCCAGCGCCACACACGCGGCGATTACGCGCT 84
Qy 31 ArgAlaGluLeuLysProValLeuPheGluGlyTrpMetAlaAsnAspIleAlaGly 50
Db 85 AGGGCTGAACCTTAACCTCTCTCTCGAAGGATGGATGCTAACGACATCGCTCCGGT 144
Qy 51 GlyGlnLeuThrThrThrAspValGluAsnPheProGlyPheProAsnGlyIleMet 70
Db 145 GGTCACTAACACACCGAGCTGAGAAATTCCTCCGGAATTCCTCCAGAGGTATTC 204
Qy 71 GlyAlaAspLeuMetAspAsnCysArgAlaGlnSerLeuArgPheGlyThrAsnIleLeu 90
Db 205 GCGATGAGCTCACTGACCAATTCCTGTAACAAATCGAGCGATTCGGTACTACGATATT 264
Qy 91 SerGluThrValThrAlaValAspPheSerAlaCysProPheArgValSerAlaAspSer 110
Db 265 ACAGAGCGGTGACGAAAGTCGATTCCTTCGAAACCGTTTAAGCTATTCACAGATTCA 324
Qy 111 ThrThrValLeuAlaAspAlaValIleValAlaThrGlyAlaValAlaArgLeuHis 130
Db 325 AAAGCCATTCCTCGCTGACGCTGTGATTCCTGCTACTGAGCTGTGGCTAGCGCTTAGC 384
Qy 131 Phe-----ProGlySerAspAlaTyTrpAsnArgGlyIleSerAlaCysAla 146
Db 385 TTCGTTGGATCTGGTGAAGGTTCTGGAGGTTCTCGAACCGTGAATCTCCGCTTGCT 444
Qy 147 ValCysAspGlyAlaAlaProIlePheArgAsnLysProIleAlaValIleGlyGly 166
Db 445 GTTTCGCGAGGAGCTGCTCCGATATTCGTAACAACTCTTCGCGGTATCGGTGAGGC 504
Qy 167 AspSerAlaMetGluGluSerAsnPheLeuThrLysTyTrpGlySerHisValTrpIle 186
Db 505 GATTGAGCAATCGAAGAACAACTTCTTCAAAATATGGATCTAAAGTGATATATTC 564
Qy 187 HisArgArgAsnThrPheArgAlaSerLysIleMetGlnAlaArgAlaLeuGluAsnPro 206
Db 565 CATAGGAGATGCTTTTAGACGCTTAAGATTAATGACGACGCGAGCTTTGTCTAATCT 624
```

```

; Sequence 37, Application US/09897425
; Publication No. US20020088025A1
; GENERAL INFORMATION:
; APPLICANT: MOLONEY, MAURICE M.
; APPLICANT: DALMIA, BIPIN K.
; TITLE OF INVENTION: PREPARATION OF THIOREDOXIN AND THIOREDOXIN REDUCTASE
; TITLE OF INVENTION: PROTEINS ON OIL BODIES
; FILE REFERENCE: 034547/0106
; CURRENT APPLICATION NUMBER: US/09/897,425
; CURRENT FILING DATE: 2001-07-03
; PRIOR FILING DATE: 09/210,843
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 08/846,021
; PRIOR FILING DATE: 1997-04-25
; PRIOR APPLICATION NUMBER: 08/366,793
; PRIOR FILING DATE: 1994-12-30
; PRIOR APPLICATION NUMBER: 08/142,418
; PRIOR FILING DATE: 1993-11-16
; PRIOR APPLICATION NUMBER: 07/659,835
; PRIOR FILING DATE: 1991-02-22
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 37
; LENGTH: 1002
; TYPE: DNA
; ORGANISM: Arabidopsis sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(999)
; US-09-897-425-37

Alignment Scores:
Pred. No.: 5,01e-160 Length: 1002
Score: 1318.00 Matches: 254
Percent Similarity: 86.77% Conservative: 28
Best Local Similarity: 78.15% Mismatches: 39
Query Match: 77.12% Indels: 4
DB: 13 Gaps: 1

US-10-005-429-25 (1-331) x US-09-897-425-37 (1-1002)

Qy 11 ThrArgIleCysIleIleGlySerGlyProAlaAlaHisThrAlaAlaIleTyrAlaAla 30
Db 25 ACAGAGCTCTGTATCGTAGAGAGTGGCCACCGGCGCACACACGGCGGATTTACGAGCT 84
Qy 31 ArgAlaGluLeuLysProValLeuPheGluGlyTyrMetAlaAsnAspIleAlaAlaGly 50
Db 85 AGGGCTGAACCTTAACCTCTCTCTTCGAAGAGTGGATGGCTAACGACATCGCTCCCGGT 144
Qy 51 GlyGlnLeuThrThrThrAspValGluAsnPheProGlyPheProAsnGlyIleMet 70
Db 145 GGTCAACTAAACACACACCGACGTCGAGAAATTTCCCGGATTTCCGAAAGGATTTCTC 204
Qy 71 GlyAlaAspLeuMetAspAsnCysArgAlaGlnSerLeuArgPheGlyThrAsnIleLeu 90
Db 205 GGAGTAGAGCTCAGTACAAATTCGTAAACAAATCGGAGCGATTCGGTACTACGATATT 264
Qy 91 SerGluThrValThrAlaValAspPheSerAlaCysProPheArgValSerAlaAspSer 110
Db 265 ACAGAGAGCGTACGAAAGTGGATTTCTTCGAAACCGGTTTAAGCTATTACAGATTTCA 324
Qy 111 ThrThrValLeuAlaAspAlaValIleValAlaThrGlyValAlaAlaArgLeuHis 130
Db 325 AAAGCATTCCTCGTACGCTGTGATTCCTCGTACTGGAGCTGTGGCTAAGCGGCTTAGC 384
Qy 131 Phe-----ProGlySerAspAlaTyrTyrAsnArgGlyIleSerAlaCysAla 146
Db 385 TTCGTTGGATCTGGTGAAGGTTCTGGAGGTTTCTGGAACCGTGGAAATCTCGGCTTGCT 444
Qy 147 ValCysAspGlyAlaAlaProIlePheArgAsnLysProIleAlaValIleGlyGly 166
Db 445 GTTTCGAGGAGCTGCTCCGATATTCGTACAAACCTCTTGGCTGATTCGGTGGAGGC 504

```

```

167 AspSerAlaMetGluGluSerAsnPheLeuThrLysTyrGlySerHisValTyrIleIle 186
505 GATTCAGCAATGGAGAGCAAACTTCTTCAAAATATGGATCTAAAGGTATATATATC 564
187 HisArgAsnThrPheArgAlaSerLysIleMetGlnAlaAlaArgAlaLeuGluAsnPro 206
565 CATAGGAGAGATCTTTTAGAGCGTCTAAGATTATGACGACGAGCTTTGTCTAATCCT 624
207 LysIleLysValLeuThrAspSerGluValValGluAlaTyrGlyGlyAlaAsnGlyGly 226
625 AAGATTGATGTGATTGGAACTCGTCTGTTGTGAAGCTTATGGAGATGGAGAAAGAGAT 684
227 ProLeuAlaGlyValLysValLysAsnLeuLeuAsnGlyGluValSerAspLeuGlnVal 246
685 GTGCTGGAGGATTGAAGTGAAGAATGTGTTACCGAGATGTTTCTGATTTAAAAAGTT 744
247 SerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLysPheLeuGlyGlnLeu 266
745 TCTGGATTGTCTTCTGTTGTCATGTCAGAGCCAGTACCAAGTTTGTGATGTGTGT 804
267 GluLeuAspSerAspGlyTyrValGluThrLysProGlySerThrHisThrSerValLys 286
805 GAGTTAGATTGGATGGTTATGTTGTCAGAGCGCTGGTACTACACAGACTAGCGTTCC 864
287 GlyValPheAlaAlaGlyAspValGlnAspLysLysTyrArgGlnAlaIleThrAlaAla 306
865 GGAGTTTTCGCTCGGGTGATGTTTCAGGATAAGAGTATAGGCAAGCCATCCTGCTGCA 924
307 GlySerGlyCysMetAlaAlaLeuAspAlaGluHisTyrLeuGlnGluIleGlyAlaGln 326
925 GGAACCTGGTGTCATGGCAGCTTTGGATGACAGACATTACTTACAGAGATTGGATCTCAG 984
327 GluGlyLysSerAsp 331
985 CAAGGTAAGAGTGTAT 999

RESULT 13
US-10-032-201B-8
; Sequence 8, Application US/10032201B
; Publication No. US20030167524A1
; GENERAL INFORMATION:
; APPLICANT: Van Rooijen, Gij's
; APPLICANT: Heifetz, Peter Bernard
; APPLICANT: Briggs, Steven
; APPLICANT: Dalmia, Bipin Kumar
; APPLICANT: Del Val, Greg
; APPLICANT: Zaplachinski, Steve
; APPLICANT: Moloney, Maurice
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED
; FILE REFERENCE: 38814 351B
; CURRENT APPLICATION NUMBER: US/10/032,201B
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 313
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 1002
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; US-10-032-201B-8

Alignment Scores:
Pred. No.: 5,01e-160 Length: 1002
Score: 1318.00 Matches: 254
Percent Similarity: 86.77% Conservative: 28
Best Local Similarity: 78.15% Mismatches: 39
Query Match: 77.12% Indels: 4
DB: 15 Gaps: 1

US-10-005-429-25 (1-331) x US-10-032-201B-8 (1-1002)

Qy 11 ThrArgIleCysIleIleGlySerGlyProAlaAlaHisThrAlaAlaIleTyrAlaAla 30

```


Db 565 CATAGGAGAGATGCTTTAGAGCGTCTAAGATTATGACAGCGAGCTTTGCTAATCCT 624
Qy 207 LysileLeuValLeuThrAspSerGluValValGluAlaThrGlyGly 226
Db 625 AAGATTGATGCTATTTGGAACTGCTGTTGTGGAACTTATGGAGATGGAGAAGAGAT 684
Qy 227 ProLeuAlaGlyValLysValLysAsnLeuAsnGlyGluValSerAspLeuGlnVal 246
Db 685 GTGCTTGGAGGATTGAAGTGAAGATGTTGTTACCGGAGATGTTCTGATTTAAAGTT 744
Qy 247 SerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLysPheLeuGlyGlnLeu 266
Db 745 TCTGGATTGCTTCTTCTGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCT 804
Qy 267 GluLeuAspSerAspGlyTyrValGluThrLysProGlySerThrHisThrSerValLys 286
Db 805 GAGTTAGATTCGATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTAT 864
Qy 287 GlyValPheAlaGlyAspValGlnAspLysLysLysLysLysLysLysLysLys 306
Db 865 GGAGTTTTCGCTCGCGGCTGATGTTTCAGGATAAGAGTATAGGCAAGCCATCATCTGCTGCA 924
Qy 307 GlySerGlyCysMetAlaAlaLeuAspAlaGluHisTyrLeuGlnGlyAlaGln 326
Db 925 GGAACCTGGGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 984
Qy 327 GluGlyLysSerAsp 331
Db 985 CAAGGTAAGAGTGAAT 999

RESULT 11

US-09-897-425-36
; Sequence 36, Application US/09897425
; Publication No. US20020688025A1
; GENERAL INFORMATION:
; APPLICANT: MOLONEY, MAURICE M.
; APPLICANT: DALMA, BIPIN X.
; TITLE OF INVENTION: PREPARATION OF THIOREDIXIN AND THIOREDIXIN REDUCTASE
; TITLE OF INVENTION: PROTEINS ON OIL BODIES
; FILE REFERENCE: 034547/0106
; CURRENT APPLICATION NUMBER: US/09/897,425
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 09/210,843
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 08/846,021
; PRIOR FILING DATE: 1997-04-25
; PRIOR APPLICATION NUMBER: 08/366,783
; PRIOR FILING DATE: 1994-12-30
; PRIOR APPLICATION NUMBER: 08/142,418
; PRIOR FILING DATE: 1993-11-16
; PRIOR APPLICATION NUMBER: 07/659,835
; PRIOR FILING DATE: 1991-02-22
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 1002
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Published NADPH
; OTHER INFORMATION: thioredoxin reductase sequence
; NAME/KEY: CDS
; LOCATION: (1)..(999)
US-09-897-425-36

Alignment Scores:
Pred. No.: 5,01e-160 Length: 1002
Score: 1318.00 Matches: 254
Percent Similarity: 86.77% Conservative: 28
Best Local Similarity: 78.15% Mismatches: 39
Query Match: 77.12% Indels: 4
DB: 13 Gaps: 1

US-10-005-429-25 (1-331) x US-09-897-425-36 (1-1002)
Qy 11 ThrArgileCysIleIleGlySerGlyProAlaAlaHisThrAlaAlaIleTyrAlaAla 30
Db 25 ACAAGGCTCTGTATCGTAGGAAGTGGCCAGCGGCACACACCGCGCGCATTTTACCAGCT 84
Qy 31 ArgAlaGluLeuLysProValLeuPheGluGlyTyrMetAlaAsnAspIleAlaAlaGly 50
Db 85 AGGGCTGAACCTTAAACCTCTCTCTTCGAAGATGATGGCTAACGACATGCTCCCGT 144
Qy 51 GlyGlnLeuThrThrThrThrAspValGluAsnPheProGlyPheProAsnGlyIleMet 70
Db 145 GGTCACTAACACACACCGACGCTCGAGAATTTCCCGCGATTTCCAGAAAGTATTCTC 204
Qy 71 GlyAlaAspLeuMetAspAsnCysArgAlaGlnSerLeuArgPheGlyThrAsnIleLeu 90
Db 205 GAGTAGAGCTCAGTGAACAATTCGTAAACATCGGAGCGATTTCGGTACTACGATATT 264
Qy 91 SerGluThrValThrAlaValAspPheSerAlaCysProPheArgValSerAlaAspSer 110
Db 265 ACAGAGACGGTGACCAAAAGTTCGATTCTCTTCGAAACCGTTTAAAGCTATTCACAGATTCA 324
Qy 111 ThrThrValLeuAlaAspAlaValIleValAlaThrGlyAlaValAlaAlaArgArgLeuHis 130
Db 325 AAAGCCATCTCTCGCTGACGCTGTGATTCTCGCTACTGGAGCTGTGGCTAAGCGGTAGC 384
Qy 131 Phe-----ProGlySerAspAlaTyrTyrAsnArgGlyIleSerAlaCysAla 146
Db 385 TTCGTTGGATCTGGTGAAGTTCTCGAGGTTCTCGAACCGTGAATCTCCGCTTGTGCT 444
Qy 147 ValCysAspGlyAlaAlaPheArgLeuPheProIleAlaValIleGlyGlyGly 166
Db 445 GTTTCGACGGAGCTGCTCCGATATTCGTAAACACCTCTTCGCGTGATCCGTTAGGAGC 504
Qy 167 AspSerAlaMetGluGluSerAsnPheLeuThrLysTyrGlySerHisValTyrIleIle 186
Db 505 GATTCAAGCAATGGAAGAAGCAAACTTCTTCAAAATATGGATCTAAAGTGTATATAATC 564
Qy 187 HisArgArgAsnThrPheArgAlaSerLysIleMetGlnAlaArgAlaLeuGluAsnPro 206
Db 565 CATAGGAGAGATGCTTTTAGAGCGTCTAAGATTATGCGACGACGAGCTTTGCTAATCCT 624
Qy 207 LysIleLysValLeuTyrAspSerGluValValGluAlaTyrGlyAlaAsnGlyGly 226
Db 625 AAGATTGATGTTGATTGGAACTCGTCTGTTGGAGCTTATGGAGATGGAGAAGAGAT 684
Qy 227 ProLeuAlaGlyValLysValLysAsnLeuLeuAsnGlyGluValSerAspLeuGlnVal 246
Db 685 GTGCTTGGAGGATTGAAAGTGAAGATGTTGTTACCGGAGATGTTTCTGATTTAAAGTT 744
Qy 247 SerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLysPheLeuGlyGlnLeu 266
Db 745 TCTGGATTGCTTCTTGTCTATTGCTCATGAGCCAGCTACCAAGTTTGTGATGGTGTGT 804
Qy 267 GluLeuAspSerAspGlyTyrValGluThrLysProGlySerThrHisThrSerValLys 286
Db 805 GAGTTAGATTCGATGCTTATGTTGTGTCAGAACCTGTTACTACACAGACTAGCTTCC 864
Qy 287 GlyValPheAlaAlaGlyAspValGlnAspLysLysLysLysLysLysLysLysLys 306
Db 865 GGAGTTTTCGCTCGCGGCTGATGTTTCAGGATAAGAGTATAGGCAAGCCATCATCTGCTGCA 924
Qy 307 GlySerGlyCysMetAlaAlaLeuAspAlaGluHisTyrLeuGlnGlyAlaGln 326
Db 925 GGAACCTGGGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 984
Qy 327 GluGlyLysSerAsp 331
Db 985 CAAGGTAAGAGTGAAT 999

RESULT 12

US-09-897-425-37

```

145 GGTCACTACACACCCAGCGTCCGAGATTTCCCGGATTTCCAGAGGTTATTC 204
Qy 71 GlyAlaSerLeuMetAspAsnGlnSerLeuArgPheGlyThrAsnIleLeu 90
Db 205 GGAGTAGAGCTCACTGACAAATTCGTAACATTCGGAGCGATTCGGTACTACGATTT 264
Qy 91 SerGluThrValThrAlaValAspPheSerAlaCysProPheArgValSerAlaAspSer 110
Db 265 ACAGAGCGGTGACGAAAGTCGATTTCTTCGAAACCGTTAAGCTATTCCACAGATTC 324
Qy 111 ThrThrValLeuAlaAspAlaValIleValAlaThrGlyAlaValAlaArgLeuHis 130
Db 325 AAAGCCATTCCTCGCTGCGTGTGATTTCTGCTACTGAGCTGTGGCTAAGCGGCTTAGC 384
Qy 131 Phe-----ProGlySerAspAlaThrPheAsnArgGlyIleSerAlaCysAla 146
Db 385 TTCCTTGATCTGCTGAGGTTCTGAGGTTCTCGAACCGTTAAGCTATTCCAGATTC 444
Qy 147 ValCysAspGlyAlaAlaProIlePheArgAsnLysProIleAlaValIleGlyGly 166
Db 445 GTTTCGACGAGCTGCTCGATATTCGTAACCAACCTCTTGGGCTGATCGGTGGAGGC 504
Qy 167 AspSerAlaMetGluGluSerAsnPheLeuThrLysTyrGlySerHisValTyrIle 186
Db 505 GATTACAGCAATGGAAGACCAATCTTCTTACAAATATGGAATTAAGTGTATATAATC 564
Qy 187 HisArgAsnThrPheArgAlaSerLysIleMetGlnAlaArgAlaLeuGluAsnPro 206
Db 565 CATAGGAGAGATCTTTAGAGCTCTAAGATTATGACGAGCGAGCTTTGCTTAATCCT 624
Qy 207 LysIleLysValLeuThrAspSerGluValValGluAlaThrGlyAlaAsnGlyGly 226
Db 625 AAGATTGATGTGATTTGGAATCTGCTCTGTTGGAAGCTTATGAGATGGGAAAGAGAT 684
Qy 227 ProLeuAlaGlyValLysValLysAsnLeuLeuAsnGlyGluValSerAspLeuGlnVal 246
Db 685 GTGCTTGAGGATTCGAAGTGAAGATCTGTTACCGGAGATGTTCTGATTTAAAGTT 744
Qy 247 SerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLysPheLeuGlyGlyGlnLeu 266
Db 745 TCTGGATGTTCTTTGCTATTTGCTCATGAGCCAGCTACCAAGTTTTCGATGGTGGT 804
Qy 267 GluLeuAspSerAspGlyTyrValGluThrLysProGlySerThrHisThrSerValLys 286
Db 805 GAGTTAGATTCGATGGTATGTTGTCAGAGGCTGTGATACACAGACTAGCGTTCCC 864
Qy 287 GlyValPheAlaAlaGlyAspValGlnAspLysLysTyrArgGlnAlaIleThrAlaAla 306
Db 865 GGAGTTTTCGCTGCGGTGATGTTTTCAGATAAAGATATAGCAAGCCATCACTGCTGCA 924
Qy 307 GlySerGlyCysMetAlaAlaLeuAspAlaGluHisTyrLeuGlnGluIleGlyValGln 326
Db 925 GGAAGTGGTGCATGGGAGCTTTGATGACAGGATTTTACAGAGATTTGGATCTCAG 984
Qy 327 GluGlyLysSerAsp 331
Db 985 CAAGGTAAAGATGAT 999

```

RESULT 10

```

US-09-897-898-2
; Sequence 2, Application US/09897898
; Patent No. US2002003703A1
; GENERAL INFORMATION:
; APPLICANT: DECKERS, HARM M.
; APPLICANT: VAN ROOIJEN, GIJS
; APPLICANT: BOOTHE, JOSEPH
; APPLICANT: GOLLI, JANIS
; APPLICANT: MOLONEY, MAURICE M.
; APPLICANT: DALMIA, BIPIN K.
; TITLE OF INVENTION: THIOREDOLIN AND THIOREDOLIN REDUCTASE CONTAINING OIL
; FILE OF INVENTION: BODY BASED PRODUCTS
; FILE REFERENCE: 034547/0104
; CURRENT APPLICATION NUMBER: US/09/897,898

```

```

; CURRENT FILING DATE: 2001-09-21
; PRIOR FILING DATE: 09/577,147
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: 09/448,600
; PRIOR FILING DATE: 1999-11-24
; PRIOR APPLICATION NUMBER: 09/084,777
; PRIOR FILING DATE: 1998-05-27
; PRIOR APPLICATION NUMBER: 60/047,753
; PRIOR FILING DATE: 1997-05-27
; PRIOR APPLICATION NUMBER: 60/047,779
; PRIOR FILING DATE: 1997-05-28
; PRIOR APPLICATION NUMBER: 60/075,863
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/075,864
; PRIOR FILING DATE: 1998-02-25
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1002
; TYPE: DNA
; ORGANISM: Arabidopsis sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(999)
US-09-897-898-2

```

```

Alignment Scores:
Pred. No.: 5,01e-160 Length: 1002
Score: 1318.00 Matches: 254
Percent Similarity: 86.77% Conservatives: 28
Best Local Similarity: 78.15% Mismatches: 39
Query Match: 77.12% Indels: 4
DB: 9 Gaps: 1

```

US-10-005-429-25 (1-331) x US-09-897-898-2 (1-1002)

```

Qy 11 ThrArgIleCysIleIleGlySerGlyProAlaAlaHisThrAlaIleTyrAlaAla 30
Db 25 ACAGGCTCTGATCTGATGAGAGTGGCCAGCGGACACACACGCGGCGATTTACGCGACT 84
Qy 31 ArgAlaGluLeuLysProValLeuPheGluGlyTyrMetAlaAsnAspIleAlaAlaGly 50
Db 85 AGGCGTGAATTAACCTCTCTTCGAGGAGTGGATGCTTAACGACATCGCTCCCGGT 144
Qy 51 GlyGlnLeuThrThrThrAspValGluAsnPheProGlyPheProAsnGlyIleMet 70
Db 145 GGTCACTAACCAACCCAGCTGAGATTTCCCGGATTTCCAGAGGATTTCTC 204
Qy 71 GlyAlaAspLeuMetAspAsnGlnSerLeuArgPheGlyThrAsnIleLeu 90
Db 205 GGAGTAGAGCTCACTGACAAATTCGTAACATTCGAGCGATTCGATACGATATT 264
Qy 91 SerGluThrValThrAlaValAspPheSerAlaCysProPheArgValSerAlaAspSer 110
Db 265 ACAGAGCGGTGACGAAAGTCGATTTCTCTCGAAACCGTTAAGCTATTCCACAGATTC 324
Qy 111 ThrThrValLeuAlaAspAlaValIleValAlaThrGlyAlaValAlaArgLeuHis 130
Db 325 AAAGCCATTCCTCGCTGAGCTGTGATTTCTGCTACTGAGCTGTGGCTAAGCGGCTTAGC 384
Qy 131 Phe-----ProGlySerAspAlaThrPheAsnArgGlyIleSerAlaCysAla 146
Db 385 TTCCTTGATCTGCTGAGGTTCTGAGGTTCTCGAACCGTTAAGCTATTCCAGATTC 444
Qy 147 ValCysAspGlyAlaAlaProIlePheArgAsnLysProIleAlaValIleGlyGly 166
Db 445 GTTTCGACGAGCTGCTCGATATTCGTAACCAACCTCTTGGGCTGATCGGTGGAGGC 504
Qy 167 AspSerAlaMetGluGluSerAsnPheLeuThrLysTyrGlySerHisValTyrIle 186
Db 505 GATTACAGCAATGGAAGACCAATCTTCTTACAAATATGGAATTAAGTGTATATAATC 564
Qy 187 HisArgAsnThrPheArgAlaSerLysIleMetGlnAlaArgAlaLeuGluAsnPro 206

```

```
? ORGANISM: Glycine max
? FEATURE:
? OTHER INFORMATION: Clone ID: PAT_MRT3847_30236C.1
US-10-424-599-65583

Alignment Scores:
Pred. No.: 9,1e-160 Length: 1645
Score: 1318.50 Matches: 253
Percent Similarity: 88.38% Conservative: 36
Best Local Similarity: 77.37% Mismatches: 33
Query Match: 77.15% Indels: 5
DB: 13 Gaps: 2

US-10-005-429-25 (1-331) x US-10-424-599-65583 (1-1645)
QY 10 ArgThrArgIleCysIleIleGlySerGlyProAlaAlaHisThrAlaAlaIleTyrAla 29
DB 166 ARGACCAAACTCTGCATCTCGAAGCGGTCTCTCCGCCACACACGCGCGTCTAGCGC 225
QY 30 AlaArgAlaGluLeuLysProValLeuPheGluGlyTyrMetAlaAsnAspIleAlaAla 49
DB 226 GCTCGAGCGAGCTGAAGCGCATCTCTTCGAGGGCTGGATGSCCAACGACATCGCCGCC 285
QY 50 GlyGlyGlnLeuThrThrThrThrAspValGluAsnPheProGlyPheProAsnGlyIle 69
DB 286 GCGGCGCAGCTACCAACACCCAGCGAGCTCGAGAACTTCCCGGGTTCCCGAGCGCATC 345
QY 70 MetGlyAlaAspLeuMetAspAsnCysArgAlaGlnSerLeuArgPheGlyThrAsnIle 89
DB 346 CTCGCGCGGAGCTCATAGAAAGCTCCCGAGGAGCAGTCGCTCGCTTCGGCACCGAGATC 405
QY 90 LeuSerGluThrValThrAlaValAspPheSerAlaCysProPheArgValSerAlaAsp 109
DB 406 CACCCGAGACGCTCTCCAGGTCTGATTTCTCGAACCGTCTTTCAGGGTTTTCACCGAT 465
QY 110 SerThrThrValLeuAlaAspAlaValIleValAlaThrGlyAlaValAlaArgGluLeu 129
DB 466 TCCGCAAGCGTCGAGCGCAATCCGTCATCGTCGCCACCGCGCGCTCGCAAGCGCCTC 525
QY 130 HisPheProGlySer-----AspAlaTyrTrpAsnArgGlyIleSerAlaCys 145
DB 526 CCTCTCCCGGCTCCGCGAGTCGCCCGGAGTCTGGAACCGCGGATCTCCGCGTGC 585
QY 146 AlaValCysAspGlyAlaAlaProIlePheArgAsnLysProIleAlaValIleGlyIle 165
DB 586 GCGCTCTGCGATGCGCGCGCGCGATCTTCGGAACCAAGCCTAGCGGTGATCGCGCGC 645
QY 166 GlyAspSerAlaMetGluSerAsnPheLeuThrIleGlySerHisValTyrIle 185
DB 646 GGGGATCGCGCGATGAGGAGCGCCCTCTCTCCCAAGTACGTTCCGAGGTTTACATA 705
QY 186 IleHisArgAsnThrPheArgAlaSerLysIleMetGlnAlaArgAlaLeuGluAsn 205
DB 706 ATTCCCGGAGGATACATTCAGGGCTTCGAAGATTATCGAGCAAGGTTATGGCAAT 765
QY 206 ProLysIleLysValLeuTrpAspSerGluValValGluAlaTyrGlyAla---Asn 224
DB 766 AGCAGATTAAAGTGATTTGGAATTCCGTTGGTGGTTGAGGCTTTTGGGGCGGAGATAAC 825
QY 225 GlyGlyProLeuAlaGlyValLysValIleAsnLeuAsnGlyGluValSerAspLeu 244
DB 826 AGAGGGTGCTTGGGGATTGAGGGTGAAGAATGTGCTGCTCGAGGATGTTCTGATTTG 885
QY 245 GlnValSerGlyLeuPheAlaIleGlyHisGluProAlaThrLysPheLeuGlyGly 264
DB 886 AAGTTCTTGGGTGTTTTCGCAATTGGCAGCGCCCGCAGCCCAAGTTCTTGGACGGG 945
QY 265 GlnLeuGluLeuAspSerAspGlyTyrValGluThrIleProGlySerThrHisThrSer 284
DB 946 CAGCTTGAATTGATTTCTGATGATATATTGTGACGAAGCCGGGAGGAGCAAGACAGT 1005
QY 285 ValLysGlyValPheAlaAlaGlyAspValGlnAspLysLysTyrArgGlnAlaIleThr 304
```

```
DB 1006 GTTAGGGAGGTTTGTCTGCTGGGGATGTTTCAGGACAGAAAGTATAGGCAAGCTATTACT 1065
QY 305 AlaAlaGlySerGlyCysMetAlaAlaLeuAspAlaGluHisTyrLeuGlnGluIleGly 324
DB 1066 GCTGCTGGCACTGGATGATGCTGCTTTGGATGTCAGAACATTACTTGCACAAATGTTGCT 1125
QY 325 AlaGlnGluGlyLysSerAsp 331
DB 1136 TTACAACAAGATAGAGTGAT 1146
RESULT 9
US-09-897-898-1
; Sequence 1, Application US/09897898
; Patent No. US20020037303A1
; GENERAL INFORMATION:
; APPLICANT: DECKERS, HARM M.
; APPLICANT: VAN ROOIJEN, GIJS
; APPLICANT: BOOTHE, JOSEPH
; APPLICANT: GOLD, JANIS
; APPLICANT: MOLONEY, MAURICE M.
; APPLICANT: DALMA, BIPIN K.
; TITLE OF INVENTION: THIOREDOLIN AND THIOREDOLIN REDUCTASE CONTAINING OIL
; TITLE OF INVENTION: BODY BASED PRODUCTS
; FILE REFERENCE: 034547/0104
; CURRENT APPLICATION NUMBER: US/09/897,898
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 09/577,147
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: 09/448,600
; PRIOR FILING DATE: 1999-11-24
; PRIOR APPLICATION NUMBER: 09/084,777
; PRIOR FILING DATE: 1998-05-27
; PRIOR APPLICATION NUMBER: 60/047,753
; PRIOR FILING DATE: 1997-05-27
; PRIOR APPLICATION NUMBER: 60/047,779
; PRIOR FILING DATE: 1997-05-28
; PRIOR APPLICATION NUMBER: 60/075,863
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/075,864
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatensIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1002
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(999)
; OTHER INFORMATION: Description of Unknown Organism: Published NADPH
; OTHER INFORMATION: thioredoxin reductase
; US-09-897-898-1
Alignment Scores:
Pred. No.: 5,01e-160 Length: 1,002
Score: 1318.00 Matches: 254
Percent Similarity: 86.77% Conservative: 28
Best Local Similarity: 78.13% Mismatches: 39
Query Match: 77.12% Indels: 4
DB: 9 Gaps: 1
US-10-005-429-25 (1-331) x US-09-897-898-1 (1-1002)
QY 11 ThrArgIleCysIleIleGlySerGlyProAlaAlaHisThrAlaAlaIleTyrAlaAla 30
DB 25 ACAGGCTCTGTATGTAGGAAGTGGCCAGCGGCACACACCGCGCGATTACGAGCT 84
QY 31 ArgAlaGluLeuLysProValLeuPheGluGlyTyrMetAlaAsnAspIleAlaAlaGly 50
DB 85 AGGGCTGACTTAACTCTCTCTCGAAGGATGATGCTTAACGACATCGCTCCCGGT 144
QY 51 GlyGlnLeuThrThrThrThrAspValGluAsnPheProGlyPheProAsnGlyIleMet 70
```



```

QY 1 MetGluGlySerAlaAlaAlaProLeuArgThrArgIleCysIleIleGlySerGlyPro 20
Db 406 ATGGAGGATCCCGCGGGGCGGCTCCGACGCGCTGTGATCATCGGAGCGGGCG 465
QY 21 AlaAlaHisThrAlaAlaIleTyrAlaAlaArgAlaGluLeuLysProValLeuPheGlu 40
Db 466 TCGGGGACACGCGCGGATCTACGCGCGCGCGGAGCTCAAGCGCGCTGTCTCTCGAG 525
QY 41 GlyTyrMetAlaAsnAspIleAlaAlaGlyGlyGlnLeuThrThrThrThrThrThrThr 60
Db 526 GGTCTGCTCGCCACACGATTCGCGCGCGGGGGGCGAGCTCACACACACACGCGCTCGAG 585
QY 61 AsnPheProGlyPheProAsnGlyIleMetGlyAlaAspLeuMetAspAsnCysArgAla 80
Db 586 AACTTCCCGGGTTCCTCCGAGGGATCTCCGCGCGGAGCTCATGATCGTGGCGCGCC 645
QY 81 GlnSerLeuArgPheGlyThrAsnIleLeuSerGluThrValThrAlaValAspPheSer 100
Db 646 CAGTCCCTCCGGTTCGGCCAGCATCTCCGACCGCTCACCGCGTCACTCTCC 705
QY 101 AlaCysProPheArgValSerAlaAspSerThrThrValLeuAlaAspAlaValIleVal 120
Db 706 GCCCGCCCTTCGGCGTCCCTCCGACTCCACACCGTCTCGCGAGCGCGTGGTGGTC 765
QY 121 AlaThrGlyAlaValAlaArgLeuHisPheProGlySerAspAlaTyrTrpAsnArg 140
Db 766 GCCACGGGCGCGTCCCGCGGAGCTCCACTTCGCGGCTCCGACGCTTACTGGAACCGC 825
QY 141 GlyIleSerAlaCysAlaValCysAspGlyAlaAlaProIlePheArgAsnLysProIle 160
Db 826 GGCATCTCAGCTGCGCGCTCTCGAGCGGGCGCGCCCAATCTTCAGGAACAAACCCATC 885
QY 161 AlaValIleGlyGlyGlyAspSerAlaMetGluSerAsnPheLeuThrLysTyrGly 180
Db 886 GCGCTCATCGCGCGCGGACTCCGCGCATCGGAGGATCCAACTTCTCCACCAAGTAACGC 945
QY 181 SerHisValTyrIleIleHisArgArgAsnThrPheArgAlaSerLysIleMetGlnAla 200
Db 946 TCCATGTGTATCATATCATCCCGCCGACACACCTTCGCGGCTCCCAAGATCATGAGGCGC 1005
QY 201 ArgAlaLeuGluAsnProLysIleLysValLeuTrpAspSerGluValValGluAlaTyr 220
Db 1006 AGGGCGTGTCAAACCCCAAGATCCAGGTTTCTGGGACTCTGAGGTCGTCGAGGCGCTAC 1065
QY 221 GlyGlyAlaAsnGlyGlyProLeuAlaGlyValLysValLysValLysValLysValLys 240
Db 1066 GCGCGGAGGCTGAGGCTCATTTGGCTGGTGTCAAGGTGAAGACTTTGGTTACTGGGAAG 1125
QY 241 ValSerAspLeuGlnValSerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLys 260
Db 1126 ATCTCCGACCTTCAGGTGTCGCGTCTCTCTTCGCGCATCGGACATCAACCGCGACGAG 1185
QY 261 PheLeuGlyGlyGlnLeuGluLeuAspSerAspGlyTyrValGluThrLysProGlySer 280
Db 1186 TTCTCGCGGGGAGCTTGAAGGGGCTTTTGTGCTGGGTATGTGGCCACCAAGCGAGCTCC 1245
QY 281 ThrHisThrSerValLysGlyValPheAlaAlaGlyAspValGlnAspLysLysTyrArg 300
Db 1246 ACCACACACAGTGTGAAGGGGCTTTTGTGCTGGGGA1GTGACGACGAAGATATCGC 1305
QY 301 GlnAlaIleThrAlaAlaGlySerGly 309
Db 1306 CAGGCTATTACTCCGCGTGGATCAGGT 1332

```

RESULT 6
 US-09-938-842A-2486
 ; Sequence 2486, Application US/09938842A
 ; Patent No. US20020160378A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Harper, Jeff
 ; APPLICANT: Kreps, Joel
 ; APPLICANT: Wang, Xun
 ; APPLICANT: Zhu, Tong

```

; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 2486
; LENGTH: 1152
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; US-09-938-842A-2486

Alignment Scores:
Pred. No.: 3,38e-162 Length: 1152
Score: 1335.50 Matches: 258
Percent Similarity: 86.65% Conservative: 34
Best Local Similarity: 76.56% Mismatches: 36
Query Match: 78.15% Indels: 9
DB: 9 Gaps: 2

US-10-005-429-25 (1-331) x US-09-938-842A-2486 (1-1152)
QY 4 SerAlaAlaAlaProLeu-----ArgThrArgIleCysIleIleGlySer 18
Db 139 TCCGCGCGCGCGCGCTCGACATGGAACCTCAAAAACCAAGGTTTGCATCGTCGGAAGT 198
QY 19 GlyProAlaAlaHisThrAlaAlaIleTyrAlaAlaArgAlaGluLeuLysProValLeu 38
Db 199 GGACGAGGAGGACACACGCGCGCGGATCTATGATCATGAGAGCGAGCTTAAGGCTCTTCTC 258
QY 39 PheGluGlyTyrMetAlaAsnAspIleAlaAlaGlyGlyGlnLeuThrThrThrThrThr 58
Db 259 TTCGAGGATGGATGGCTTAACGACATCGCTCCGCGCGGTCAATTAACTACAAACACCGAC 318
QY 59 ValGluAsnPheProGlyPheProAsnGlyIleMetGlyAlaAspLeuMetAspAsnCys 78
Db 319 GTCCGAAATCTCCCTCGGGTTCCTGAAGGTATTTCCGGTATTGATATCGTTGAGAAATTC 378
QY 79 ArgAlaGlnSerLeuArgPheGlyThrAsnIleLeuSerGluThrValThrAlaValAsp 98
Db 379 AGAAACAAATCGGAGAGATTTGGAACATGATCTTCACGGAACCTGTTAACAAAGTTGAT 438
QY 99 PheSerAlaCysProPheArgValSerAlaAspSerThrThrValLeuAlaAspAlaVal 118
Db 439 TTCTCATCGAAACCGCTTTAAGCTATTCACTGATTCGAGAACTGTTCCTCGCTGATTTCTGA 498
QY 119 IleValAlaThrGlyAlaValAlaAlaArgAlaGluLeuHisPheProGlySer----- 134
Db 499 ATCATTTCTACTGGAGCTGTGCTAAAGCTCTTAGCTTCACTGGATCTCGTGAAGGTAAT 558
QY 135 AspAlaTyrTrpAsnArgGlyIleSerAlaCysAlaValCysAspGlyAlaAlaProfile 154
Db 559 GGTGGTTTTGGATCGGTGATCTCCGCTTGTGCTGTGTTGCGAGCGAGCTGCTCGGAT 618
QY 155 PheArgAsnLysProIleAlaValIleGlyGlyAspSerAlaMetGluSerAsn 174
Db 619 TTTAGGAATAAGCCCTCTTGTGTTATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 678
QY 175 PheLeuThrLysTyrGlySerHisValTyrIleIleHisArgAsnThrPheArgAla 194
Db 679 TTTCTGACTAGTATGGATTAAGGTTTATATTATTCATAGGAGGATACGTTTAGGGCG 738
QY 195 SerLysIleMetGlnAlaArgAlaLeuGluAsnProLysIleLysValLeuTrpAspSer 214
Db 739 TCTAAGATTATCGACGAGAGCTTTGTCTAACCCCTTAAGATTGAAGTATTGGAACTCT 798
QY 215 GluValValGluAlaTyrGlyGlyAlaAsnGlyGlyProLeuAlaGlyValLysValLys 234

```

; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
 ; FILE OF INVENTION: SAME, AND METHODS OF USE
 ; FILE REFERENCE: SCRIPI300-3
 ; CURRENT APPLICATION NUMBER: US/09/938,842A
 ; CURRENT FILING DATE: 2001-08-24
 ; PRIOR APPLICATION NUMBER: US 60/227,866
 ; PRIOR FILING DATE: 2000-08-24
 ; PRIOR APPLICATION NUMBER: US 60/264,647
 ; PRIOR FILING DATE: 2001-01-16
 ; PRIOR APPLICATION NUMBER: US 60/300,111
 ; PRIOR FILING DATE: 2001-06-22
 ; NUMBER OF SEQ ID NOS: 5379
 ; SEQ ID NO 2486
 ; LENGTH: 1152
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 ; US-09-938-842A-2486

```

Db      959 GCAGGAGTGGGTGCACACAGGTGGGCAAGTCTGAT 992
US-10-091-841-23
; Sequence 23, Application US/10091841
; Publication No. US20030150010A1
; GENERAL INFORMATION:
; APPLICANT: Cho, Myeong-Je
; APPLICANT: Del Val, Greg
; APPLICANT: Caillaud, Maxime
; APPLICANT: Lemauz, Peggy G.
; APPLICANT: Buchanan, Bob B.
; TITLE OF INVENTION: Barley Gene for Thioredoxin and
; TITLE OF INVENTION: NADP-Thioredoxin Reductase
; FILE REFERENCE: 2001-0701.30
; CURRENT APPLICATION NUMBER: US/10/091,841
; CURRENT FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: 09/540,014
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 60/127,198
; PRIOR FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: US 60/169,162
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: US 60/177,740
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 60/177,739
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; TYPE: DNA
; ORGANISM: Hordeum vulgare
US-10-091-841-23

Alignment Scores:
Pred. No.: 7,49e-185 Length: 395
Score: 1510.00 Matches: 302
Percent Similarity: 93.98% Conservativeness: 10
Best Local Similarity: 90.9% Mismatches: 19
Query Match: 88.3% Indels: 3
DB: 15 Gaps: 0

US-10-005-429-25 (1-331) x US-10-091-841-23 (1-995)

Qy      1 MetGluGlySerAlaCysAlaValCysAspGlyValAlaProIlePheArgAsnLysProIle 20
Db      1 ATGGAGGGATCGCGCGCGCGCGCGCTCCGACGCGGTGTCATCATCGGAGCGGCGCG 60
Qy      21 AlaAlaHisThrAlaAlaIleThrAlaAlaArgAlaGluLeuLysProValLeuPheGlu 40
Db      61 GCCGGGCACACGCGCGCCCATCTACGCGCGCGCGCGCGGCTCAAGCGCGGTGCTCTTCGAG 120
Qy      41 GlyTrpMetAlaAsnAspIleAlaAlaGlyGlyGlnLeuThrThrThrThrThrThrThr 60
Db      121 GCTTGGATGGCCACGACATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
Qy      61 AsnPheProGlyPheProAsnGlyIleMetGlyAlaAspLeuMetAspAsnCysArgAla 80
Db      181 AACTTCCCGGATTCGCCACCGGCATCATGGGCATCGACCTCATGCAACACTGCGCGCGCG 240
Qy      81 GlnSerLeuArgPheGlyThrAsnIleLeuSerGluThrValThrAlaValAspPheSer 100
Db      241 CAGTCCGCTCGGCTTGGACCAACATCTCTCCGAGACGCTCACCGAGGTGCACTTCTCC 300
Qy      101 AlaCysProPheArgValSerAlaAspSerThrThrValLeuAlaAspAlaValIleVal 120
Db      301 GCCCGCGCGCTTCGGGTCACTCCGACCTCCGACCTCCGACCTCCGACCTCCGACCTCCG 360
Qy      121 AlaThrGlyAlaValAlaAlaArgLeuHisPheProGlySerAspAlaIleThrTrpAsnArg 140
Db      361 GCCACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 420

141 GlyIleSerAlaCysAlaValCysAspGlyValAlaProIlePheArgAsnLysProIle 160
161 AlaValIleGlyGlyGlyAspSerAlaMetGluGluSerAsnPheLeuThrLysThrGly 180
481 GCCTTCATCGCGCGCGGTGATTCGGCATGAGAGGAGGCAACTTCCTCACCAAGTACGGA 540
181 SerHisValTrpIleIleHisArgAsnThrPheArgAlaSerLysIleMetGlnAla 200
541 TCCAGTGTACATCATCCACGGCGGCAACACCTTCGCGCGCTCCCAAGATTATGAGGCT 600
201 ArgAlaLeuGluAsnProLysIleLysValLeuTrpAspSerGluValValGluAlaTrp 220
601 AGGCGGCTCTCCCAATCTAAGATCCAGGTGTCTGGGACTC-GAGGTGCTCGAGGGCTTAC 659
221 GlyValAlaAsnGlyGlyProLeuAlaGlyValLysValLysAsnLeuLeuAsnGlyGlu 240
660 GCGGTGACGCGCGCGCGCGCATTAAGTGGGTCAAGGTCAAGAACTTGGTACCTGGTGAG 719
241 ValSerAspLeuGlnValSerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLys 260
720 GTGTCTGACCTTCAGGTGTCCGGCTTTCTTCGCCATCGGCGCATGAGCGCGGCCCAAG 779
261 PheLeuGlyGlyGlnLeuGluLeuAspSerAspGlyTrpValGluThrLysProGlySer 280
780 TTTCTCAATGGGAGCTTGAGCTCCATGCGCATGGGTATGTGCCCAACAGCGCGGCTCT 839
281 ThrHisThrSerValLysGlyValPheAlaAlaGlyAspValGlnAspLysLysTrpArg 300
840 ACATATACCACTGTGGA-GGGGCTTTGCTGTGAGACGTCGAGGATAAGAAGTATCGT 898
301 GlnAlaIleThrAlaAlaGlySerGlyCysMetAlaAlaLeu-AspAlaGluHisTrpLe 320
899 CAGGCCATTACTGCTGTGATCAGGTGATGCTCTTGGACCGCGGAGCACTATCT 958

RESULT 5
US-10-306-292-26
; Sequence 26, Application US/10306292
; Publication No. US20030145347A1
; GENERAL INFORMATION:
; APPLICANT: Lahanan, Michael B.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Gadsaka, Pamela Y.
; TITLE OF INVENTION: GRAIN PROCESSING METHOD AND TRANSGENIC PLANTS USEFUL
; FILE REFERENCE: THEREIN
; FILE REFERENCE: A-31383P1
; CURRENT APPLICATION NUMBER: US/10/306,292
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: US/09/598,747
; PRIOR FILING DATE: 2000-06-21
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 26
; LENGTH: 1560
; TYPE: DNA
; ORGANISM: Oryza sativa
US-10-306-292-26

Alignment Scores:
Pred. No.: 2.02e-180 Length: 1560
Score: 1478.00 Matches: 282
Percent Similarity: 96.12% Conservativeness: 15
Best Local Similarity: 91.26% Mismatches: 12
Query Match: 86.48% Indels: 0
DB: 15 Gaps: 0

US-10-005-429-25 (1-331) x US-10-306-292-26 (1-1560)
```



```
QY 161 AlaValIleGlyGlyAspSerAlaMetGluGluSerAspPheLeuThrLysTyrGly 180
DB 567 GCCGTCATAGCGCGCGGACCTCCGCTATGAGGAGGTCCAAATTTCTCACCAGTACGGC 626
QY 181 SerHisValTyrIleIleHisArgArgSerPheArgAlaSerIleValMetGlnAla 200
DB 627 TCCACAGCTACATCATCCACCGCGCAATACCTTCGGTGTTCGAAGATCATGAGGCC 686
QY 201 ArgAlaLeuGluAspProLysIleLysValLeuThrPaspSerGluValValGluAlaTyr 220
DB 687 AGGGGCGCTTGAGAACCCCAAAATTAAGGTCTCTGGACTCGGAAGTTGTGAGGCCAT 746
QY 221 GlyGlyAlaAsnGlyProLeuAlaGlyValLysValLysValLysAsnLeuAsnGlyGlu 240
DB 747 GCGCGCGCAAAACGGCGGCCCATTTGGCTGGCGTAAAGGTTAAGAACCTACTGAATGGTGAG 806
QY 241 ValSerAspLeuGlnValSerGlyLeuPheAlaIleGlyHisGluProAlaThrLys 260
DB 807 GTCTCGAGATCTTCAGGTGTCTGGCTCTCTTCGCGCATCGGCGCATGAGCGCGGACCAAA 866
QY 261 PheLeuGlyGlyGlnLeuLeuLeuAspSerAspGlyTyrValGluThrLysProGlySer 280
DB 867 TTCTTGGCGGACAGCTTGAATTCGATTCGATGGTGTATGTGGAAACCAAGCCAGGTTC 926
QY 281 ThrHisThrSerValLysGlyValPheAlaIleGlyAspValGlnAspLysLysTyrArg 300
DB 927 ACTCACACAGGTGAAGGGTGTATTTGCTGCTGGCGAGGTGACGACGAAGAAGTACCGT 986
QY 301 GlnAlaIleThrAlaAlaGlySerGlyCysMetAlaAlaLeuAspAlaGluHisTyrLeu 320
DB 987 CAGGCCATTAATTCGCGTGCATCAGGGTGCATGGCTGCATTCGACCTGAGCACTACCTG 1046
QY 321 GlnGluIleGlyAlaGlnGluGlyLysSerAsp 331
DB 1047 CAGGAGATCGGTGCACAGGAGGAAAGTCTGAT 1079

RESULT 3
US-10-091-841-10
; Sequence 10, Application US/10091841
; Publication No. US20030150010A1
; GENERAL INFORMATION:
; APPLICANT: Cho, Myeong-Je
; APPLICANT: Del Val, Greg
; APPLICANT: Caillau, Maxime
; APPLICANT: Lemaux, Peggy G.
; APPLICANT: Buchanan, Bob B.
; TITLE OF INVENTION: Barley Gene for Thioredoxin and
; FILE OF INVENTION: NADP-Thioredoxin Reductase
; FILE REFERENCE: 2001-0701.30
; CURRENT APPLICATION NUMBER: US/10/091,841
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: 09/540,014
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 60/127,198
; PRIOR FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: US 60/169,162
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: US 60/177,740
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 60/177,739
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 995
; TYPE: DNA
; ORGANISM: Hordeum vulgare
US-10-091-841-10

Alignment Scores: 7.49e-185 Length: 995
Pred. No.: 1510.00 Matches: 302
Score:
```

```
Percent Similarity: 93.98% Conservative: 10
Best Local Similarity: 90.96% Mismatches: 19
Query Match: 88.36% Indels: 3
DB: 15 Gaps: 0

US-10-005-429-25 (1-331) x US-10-091-841-10 (1-995)

QY 1 MetGluGlySerAlaAlaAlaProLeuArgThrArgIleCysIleIleGlySerGlyPro 20
DB 1 ATGAGGGATCCGCGCGGCGCCCTCCGACGCGGTGTGCATCATCGGAGCGGCCG 60
QY 21 AlaAlaHisThrAlaAlaIleTyrAlaAlaArgAlaGluLeuLysProValLeuPheGlu 40
DB 61 GCGCGGCACACGCGGCGCATCTACGCGGCGCGCGGAGCTCAAGCGGTCTCTTCGAG 120
QY 41 GlyTyrMetAlaAsnAspIleAlaAlaGlyGlyGlnLeuThrThrThrThrAspValGlu 60
DB 121 GGCTGGATGGCAACGACATCGCGCGGCGGCGCATCTACGCGGCGCGGAGCTCAAGCGGTCTCTTCGAG 180
QY 61 AsnPheProGlyPheProAsnGlyIleMetGlyAlaAspLeuMetAspAsnCysArgAla 80
DB 181 AACTTCCCGGATTTCCCGCGCATCTATGGGCATCGACCTCATGGACAACATCGCGGCC 240
QY 81 GlnSerLeuArgPheGlyThrAsnIleLeuSerGluThrValThrAlaValAspPheSer 100
DB 241 CAGTCCGTCGCTTCGCGCACCAACATCTCTCCGAGACCGTCACCGAGGTGACTTCTCC 300
QY 101 AlaCysProPheArgValSerAlaAspSerThrThrValLeuAlaAspAlaValIleVal 120
DB 301 GCCCGCCCTTCGCGGTCACTCCGACCTCCACACCGTCTCCGCGACCGCGTGTCTGTC 360
QY 121 AlaThrGlyAlaValAlaArgLeuHisPheProGlySerAspAlaTyrTrpAsnArg 140
DB 361 GCCACGCGCGCGTCCGCGCGCTCCATTTCTCCGTTCCGACACCTACTTGGAAACCGC 420
QY 141 GlyIleSerAlaCysAlaValCysAspGlyAlaAlaProIlePheArgAsnLysProIle 160
DB 421 GGCATCTCCGCTCGCGCTGCGACGCTGCGCCCATCTTCGGAAACAGGCCATC 480
QY 161 AlaValIleGlyGlyAspSerAlaMetGluGluSerAsnPheLeuThrLysTyrGly 180
DB 481 GCGTTCATCGCGCGCGGTGATTCGCGCATGAGGAGGCAACTTCTCACCAGTACGGA 540
QY 181 SerHisValTyrIleIleHisArgArgSerPheArgAlaSerLysIleMetGlnAla 200
DB 541 TCCCAAGTGTATCATCATCCACGCGGCAACCTTCGCGCTCCAGATTTATGAGGCT 600
QY 201 ArgAlaLeuGluAsnProLysIleLysValLeuTyrAspSerGluValValGluAlaTyr 220
DB 601 AGGGCGCTCTCAATCTCAATCCAGTCCAGGTGTCTGGGACTC-GAGGTCTCGAGGCTTAC 659
QY 221 GlyGlyAlaAsnGlyProLeuAlaGlyValLysValLysAsnLeuLeuAsnGlyGlu 240
DB 660 GCGCGTGCAGCGCGCGGCCCATTAGCTGGGTCAAGGTCAAGACTTGGTGTCTGTGAG 719
QY 241 ValSerAspLeuGlnValSerGlyLeuPheAlaIleGlyHisGluProAlaThrLys 260
DB 720 GTGTCTGACCTTCAGGTGTCCGGCTTTCTTCGCGCATCGGCGCATGAGCGGCCACCAAG 779
QY 261 PheLeuGlyGlyGlnLeuLeuLeuAspSerAspGlyTyrValGluThrLysProGlySer 280
DB 780 TTTCTCAATGGGCGCTTGAAGTCCATCGCGGTATGTGGCCACCAAGCGGCTCT 839
QY 281 ThrHisThrSerValLysGlyValPheAlaAlaGlyAspValGlnAspLysTyrArg 300
DB 840 ACACATACCAAGTGTGGA-GGGGTCTTTGCTGCGAGACGTGCAGGATAAGATATCGT 898
QY 301 GlnAlaIleThrAlaAlaGlySerGlyCysMetAlaAlaLeu-AspAlaGluHisTyrLe 320
DB 899 CAGGCCATTAATTCGCTGCATCAGGTTCGATGGTGTCTTTGGGAGCGCGGCACTACT 958
QY 320 uGlnGluIleGlyAlaGlnGluGlyLysSerAsp 331
DB 995
```


US-10-425-114-5073

Alignment Scores:

Pred. No.: 2,08e-210 Length: 1286
 Score: 1709.00 Matches: 331
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 13 Gaps: 0

US-10-005-429-25 (1-331) x US-10-425-114-5073 (1-1286)

Qy 1 MetGluGlySerAlaAlaProLeuArgThrArgIleCysIleIleGlySerGlyPro 20
 Db 58 ATGGAGGATCGCGCGCTCGCTCGCGAGCGCATCTGCATCGCGAGCGGTCCC 117
 Qy 21 AlaAlaHisThrAlaAlaIleThrAlaAlaArgAlaGluLeuLysProValLeuPheGlu 40
 Db 118 GCTGGCAGACGGCGAGCGCATCTAGCGCGCGCGCGGAGCTCAAGCGCTGTGCTCTTCGAG 177
 Qy 41 GlyTrpMetAlaAsnAspIleAlaAlaGlyGlyGlnLeuThrThrThrAspValGlu 60
 Db 178 GCGTGGATGGCCACGACATCGCGCGCGCGCGGAGCTCACCACCAACCGAGGTCCGAG 237
 Qy 61 AsnPheProGlyPheProAsnGlyIleMetGlyAlaAspLeuMetAspAsnCysArgAla 80
 Db 238 AACATTCGCGGCTTCCCAACGGCATCATGGCGCGCGCGACCTCATGCACTGCGCGCG 297
 Qy 81 GlnSerLeuArgPheGlyThrAsnIleLeuSerGluThrValThrAlaValAspPheSer 100
 Db 298 CAGTCCCTGCGCTTGGACCAACATCTCTCCGAGACCGTCACCGCGCTGCATTTGCG 357
 Qy 101 AlaCysProPheArgValSerAlaAspSerThrThrValLeuAlaAspAlaValIleVal 120
 Db 358 GCGTCCCATTCGAGTTAGTGCAGACTCCCAACCGCTCTCGCGGATGCGGTATCGTT 417
 Qy 121 AlaThrGlyAlaValAlaArgArgLeuHisPheProGlySerAspAlaTyThrAsnArg 140
 Db 418 GCCACGGAGCGTGGCGCGCGCTCCATCTCCCGGGTCCGATGCATCTGGAACCGC 477
 Qy 141 GlyIleSerAlaCysAlaValCysAspGlyAlaAlaProIlePheArgAsnLysProIle 160
 Db 478 GGCATCTCGCTGTGCGCTGTGAGCGTGGCGCGCGCCCATCTTCGTAAACAGCCCATC 537
 Qy 161 AlaValIleGlyGlyValAspSerAlaMetGluGluSerAsnPheLeuThrLysTyGly 180
 Db 538 GCGGTCATAGCGCGCGGAGTCCGCTATGAGGAGTCCAAATTCCTCACCAGTACGCG 597
 Qy 181 SerHisValTyIleIleHisArgArgAsnThrPheArgAlaSerLysIleMetGlnAla 200
 Db 598 TCCACAGTCTACATCATCCACCGCGCAATACCTTCGCTGCTTCCAGATCATGCAGGCC 657
 Qy 201 ArgAlaLeuGluAsnProLysIleLysValLeuThrAspSerGluValValGluAlaTy 220
 Db 658 AGGCGCTTGAGAACCCCAAAATTAGGTCTCTGGGACTCGGAAGTTGTGAGGCCCTAT 717
 Qy 221 GlyGlyAlaAsnGlyProLeuAlaGlyValLysValLysAsnLeuLeuAsnGlyGlu 240
 Db 718 GCGCGCGCAACAGCGCGCCCATTCGCTGGCTGCTGAGTAAAGTTAGACCTACTGATGGTGAG 777
 Qy 241 ValSerAspLeuGlnValSerGlyLeuPheAlaIleGlyHisGluProAlaThrLys 260
 Db 778 GTCTCGGATCTTCAGGTCTGGCTCTTCCTTCGCCATCGGCGCATGAGCGCGCACCAAA 837
 Qy 261 PheLeuGlyGlnLeuGluLeuAspSerAspGlyTyValGluThrLysProGlySer 280
 Db 838 TTCCTGGCGGACACCTTGAACTCGATTCAGATGGTTATGTGGAAACCAACCCAGGTTC 897
 Qy 281 ThrHisThrSerValLysGlyValPheAlaAlaGlyAspValGlnAspLysLysTyArg 300
 Db 898 ACTCACACGAGTAAAGGGTGTATTGTCTGCTGCGGACGTCGACGACAAAGAGTACCGT 957
 Qy 301 GlnAlaIleThrAlaAlaGlySerGlyCysMetAlaAlaLeuAspAlaGluHisTyLeu 320

Db 958 CAGCCATTACTGCGCTGGATCAGGCTGCATGCTGCATGCTGCATGCTGCATGCTGCATG 1017
 Qy 321 GlnGluIleGlyAlaGlnGluGlyLysSerAsp 331
 Db 1018 CAGGAGATCGGTGCACAGGAGGGAAGTCTGTAT 1050
 RESULT 2
 US-10-425-114-3716
 : Sequence 3716, Application US/10425114
 : Publication No. US20040034888A1
 : GENERAL INFORMATION:
 : APPLICANT: Liu, Jingdong
 : APPLICANT: Zhou, Yihua
 : APPLICANT: Kovalic, David K.
 : APPLICANT: Screen, Steven B.
 : APPLICANT: Tabaska, Jack E
 : APPLICANT: Cao, Yongwei
 : TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
 : FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 : FILE REFERENCE: 38-21(53313)B
 : CURRENT APPLICATION NUMBER: US/10/425,114
 : CURRENT FILING DATE: 2003-04-28
 : NUMBER OF SEQ ID NOS: 73128
 : SEQ ID NO 3716
 : LENGTH: 1325
 : TYPE: DNA
 : ORGANISM: Zea mays
 : FEATURE:
 : OTHER INFORMATION: Clone ID: 700336177_FLI
 US-10-425-114-3716

Alignment Scores:

Pred. No.: 2,17e-210 Length: 1325
 Score: 1709.00 Matches: 331
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 13 Gaps: 0

US-10-005-429-25 (1-331) x US-10-425-114-3716 (1-1325)

Qy 1 MetGluGlySerAlaAlaAlaProLeuArgThrArgIleCysIleIleGlySerGlyPro 20
 Db 87 ATGGAGGATCGCGCGCTCGCTCGCGAGCGCATCTGCATCGCGAGCGGTCCC 146
 Qy 21 AlaAlaHisThrAlaAlaIleThrAlaAlaArgAlaGluLeuLysProValLeuPheGlu 40
 Db 147 GCTGCGACACGGCGAGCATCTAGCGCGCGCGCGGAGCTCAAGCGCTGTGCTCTTCGAG 206
 Qy 41 GlyTrpMetAlaAsnAspIleAlaAlaGlyGlyGlnLeuThrThrThrAspValGlu 60
 Db 207 GCGTGGATGGCCACGACATCGCGCGCGCGGAGCTCACCACCAACCGAGGTCCGAG 266
 Qy 61 AsnPheProGlyPheProAsnGlyIleMetGlyAlaAspLeuMetAspAsnCysArgAla 80
 Db 267 AACATTCGCGGCTTCCCAACGGCATCATGGCGCGCGGAGCTCATGGAACAATGCGCGCG 326
 Qy 81 GlnSerLeuArgPheGlyThrAsnIleLeuSerGluThrValThrAlaValAspPheSer 100
 Db 327 CAGTCCCTGCGCTTGGACCAACATCTCTCCGAGACCGCTCACCAGCGCTGCATTTTCG 386
 Qy 101 AlaCysProPheArgValSerAlaAspSerThrThrValLeuAlaAspAlaValIleVal 120
 Db 387 GCCTGCCATTCGAGTTAGTGCAGACTCCCAACCGCTCCGCGCATGCGGTATTCGTT 446
 Qy 121 AlaThrGlyAlaValAlaAlaArgArgLeuHisPheProGlySerAspAlaTyThrAsnArg 140
 Db 447 GCCACGGAGCGGTGCGCGCGCGCTCCATCTCCCGGGTCCGATGATGATGATGATGATG 506
 Qy 141 GlyIleSerAlaCysAlaValCysAspGlyValAlaAlaProIlePheArgAsnLysProIle 160
 Db 507 GGCATCTCCGCTGTGCGCTGTGAGCGGTGCGCGCGCCCATCTTCGCTAAACAGCCCATC 566

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 5, 2004, 04:58:09 ; Search time 452.691 Seconds
(without alignments)

3307.557 Million cell updates/sec

Title: US-10-005-429-25

Perfect score: 1709

Sequence: 1 MEGSAAPLRTRICIGSP.....AALDAHYLQETGAQEGKSD 331

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5

Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 2936184 seqs, 2261732022 residues

Total number of hits satisfying chosen parameters: 5872368

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters: -DEV=slp

-MODEL=frame_p2n.model -DB=slp

-Q=/cgn2_1/USPTO_spool_p/US10005429/runat_04052004_121651_1553/app_query.fasta_1.782

-DB=Published Applications NA -QWFI=fastap -SUFFIX=p2n.rnpb -MINMATCH=0.1

-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62

-TRANS=human40.cdi -LIST=45 -DOCLIGN=200 -THR SCORE=pct -THR MAX=100

-THR_MIN=0 -ALIGN=15 -NODE=LOCAL -OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0

-MAXLEN=200000000 -USR=US10005429@cgn_1_1_409@runat_04052004_121651_15537

-NCPUS=6 -ICPU=3 -NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100

-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5

-FCGAPOP=6 -FCGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:
13: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:
14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:
15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:
16: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:
17: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:
18: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:
19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
------------	-------	-------	--------	----	----	-------------

ALIGNMENTS

RESULT 1

US-10-425-114-5073

; Sequence 5073, Application US/10425114

; Publication No. US20040034888A1

; GENERAL INFORMATION:

; APPLICANT: Jiu, Jingdong

; APPLICANT: Zhou, Yihua

; APPLICANT: Kovalic, David K.

; APPLICANT: Screen, Steven E

; APPLICANT: Tabaska, Jack E

; APPLICANT: Cao, Jiongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with

; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53313)B

; CURRENT APPLICATION NUMBER: US/10425,114

; NUMBER OF SEQ ID NOS: 73128

; SEQ ID NO 5073

; LENGTH: 1286

; TYPE: DNA

; ORGANISM: Zea mays

; FEATURE:

; OTHER INFORMATION: Clone ID: 700447274_FLI

	1	1709	100.0	1286	13	US-10-425-114-5073	Sequence 5073, Ap
	2	1709	100.0	1325	13	US-10-425-114-3716	Sequence 3716, Ap
	3	1510	88.4	995	15	US-10-091-841-10	Sequence 20, Appl
	4	1510	88.4	995	15	US-10-091-841-23	Sequence 23, Appl
	5	1478	88.5	1560	15	US-10-306-292-26	Sequence 26, Appl
	6	1335.5	78.1	1152	9	US-09-938-842A-2486	Sequence 2486, Ap
	7	1335.5	78.1	1152	11	US-09-938-842A-2486	Sequence 2486, Ap
	8	1318.5	77.2	1645	13	US-10-424-599-65583	Sequence 65583, A
	9	1318	77.1	1002	9	US-09-897-898-1	Sequence 1, Appl
	10	1318	77.1	1002	9	US-09-897-898-2	Sequence 2, Appl
	11	1318	77.1	1002	13	US-09-897-898-36	Sequence 36, Appl
	12	1318	77.1	1002	13	US-09-897-898-37	Sequence 37, Appl
	13	1318	77.1	1002	15	US-10-032-201B-8	Sequence 8, Appl
	14	1318	77.1	1002	15	US-10-032-201B-10	Sequence 10, Appl
	15	1318	77.1	1344	13	US-10-290-072-238	Sequence 238, App
	16	1318	77.1	3787	9	US-09-897-898-13	Sequence 13, Appl
	17	1318	77.1	3787	13	US-09-897-898-48	Sequence 48, Appl
	18	1318	77.1	3787	15	US-10-032-201B-22	Sequence 22, Appl
	19	1318	77.1	4545	9	US-09-897-898-18	Sequence 18, Appl
	20	1318	77.1	4545	13	US-09-897-898-53	Sequence 53, Appl
	21	1318	77.1	4545	15	US-10-032-201B-27	Sequence 27, Appl
	22	1318	77.1	4546	9	US-09-897-898-15	Sequence 15, Appl
	23	1318	77.1	4546	13	US-09-897-898-50	Sequence 50, Appl
	24	1318	77.1	4546	15	US-10-032-201B-24	Sequence 24, Appl
	25	1318	77.1	6357	13	US-10-290-072-38	Sequence 38, Appl
	26	1318	77.1	6357	13	US-10-290-072-42	Sequence 42, Appl
	27	1318	77.1	6357	15	US-10-141-531-38	Sequence 38, Appl
	28	1318	77.1	6357	15	US-10-141-531-42	Sequence 42, Appl
	29	1316.5	77.0	1284	13	US-10-425-114-29681	Sequence 29681, A
	30	1306	76.4	6357	13	US-10-290-072-35	Sequence 35, Appl
	31	1306	76.4	6357	15	US-10-290-072-45	Sequence 45, Appl
	32	1306	76.4	6357	15	US-10-141-531-35	Sequence 35, Appl
	33	1306	76.4	6357	15	US-10-141-531-45	Sequence 45, Appl
	34	1305	76.4	6357	13	US-10-290-072-37	Sequence 37, Appl
	35	1305	76.4	6357	15	US-10-141-531-37	Sequence 37, Appl
	36	1304	76.3	1345	13	US-10-290-072-215	Sequence 215, App
	37	1304	76.3	6357	13	US-10-290-072-34	Sequence 34, Appl
	38	1304	76.3	6357	13	US-10-290-072-40	Sequence 40, Appl
	39	1304	76.3	6357	13	US-10-290-072-44	Sequence 44, Appl
	40	1304	76.3	6357	15	US-10-141-531-34	Sequence 34, Appl
	41	1304	76.3	6357	15	US-10-141-531-44	Sequence 44, Appl
	42	1304	76.3	6357	15	US-10-141-531-44	Sequence 44, Appl
	43	1303	76.2	6357	13	US-10-290-072-43	Sequence 43, Appl
	44	1303	76.2	6357	13	US-10-290-072-46	Sequence 46, Appl
	45	1303	76.2	6357	15	US-10-141-531-43	Sequence 43, Appl

Search completed: May 5, 2004, 09:02:42
Job time : 4713.61 secs

```

Db 19 AGTAACTGCTTATCTCGGTTTCAGCGCCGGCGGATACACCGCTGCTGTCTACCGCG 78
Qy 31 ArgAlaGluLeuLysProValLeuPheGluGlyTrpMetAlaAsnAspIleAlaAlaGly 50
Db 79 CGCGCCAACTGCAACCTGCTGCTGATTAACCGGC-----ATGCAAAAGGC 123
Qy 51 GlyGlnLeuThrThrThrAspValGluAsnPheProGlyPheProAsnGlyIleMet 70
Db 124 GGCACACTGACCAACACCGAAGTGGAAACTGGCTGGCGATCCAAACGATCTGACC 183
Qy 71 GlyAlaAspLeuMetAspAsnCysArgAlaGlnSerLeuArgPheGlyThrAsnIleLeu 90
Db 184 GGTCCGTTATTAAATGAGCGCATGACGACATGCGCAACAGTTTGAACACTGAGATCAAT 243
Qy 91 SerGluThrValThrAlaValAspPheSerAlaCysProPheArgValSerAlaAspSer 110
Db 244 TTGTATCATATCAACAGGTGATCTGCACAAACCGCTCGTTCGGTCTGATGGCGATTAAC 303
Qy 111 ThrThrValLeuAlaAspAlaValIleValAlaThrGlyAlaValAlaAlaArgArgLeuHis 130
Db 304 GCGCAATACACTTTCGACGCGCTGATTTGCGACCGGAGCTTCTGCACGCTATCTCGGC 363
Qy 131 PheProGlySerAspAlaTyTrpAsnArgGlyIleSerAlaCysAlaValCysAspGly 150
Db 364 CTGCCCTCTGAGAGAGCTTTAAAGCGCGTGGGTTTCTGTTGTCACCTTGCACCGGT 423
Qy 151 AlaAlaProIlePheArgAsnLysProIleAlaValIleGlyGlyGlyAspSerAlaMet 170
Db 424 TTC-----TTCATCGCACCAAGAGTTGCGGTCTGCGGTGATCGCGCGGCAATACCGCGTT 477
Qy 171 GluGlnSerAsnPheLeuThrLysTyTrpGlySerHisValTyIleIleHisArgArgAsn 190
Db 478 GAAGAGCGCGCTATCTCTCAACATCGCTTCGGAAGTGCATCTGATTCACCGCGCTGAC 537
Qy 191 ThrPheArgAlaSerLysIleMetGlnAlaArgAlaLeu-----GluAsnProLys 207
Db 538 GGTTCGCGCGGAAAGAAATCTCTATTAGCGCTGATGATAAGTGAAGTGAAGCGCAAC 597
Qy 208 IleLysValLeuTrpAspSerGluValGluAlaTyTrpGlyAlaAsnGlyGlyPro 227
Db 598 ATC---ATTCTGCACCAACCGTACGCTGGAAGAGTGCACCGCGCATCAATCGGT--- 651
Qy 228 LeuAlaGlyValLysValLysAsnLeuLeuAsnGlyGlu---ValSerAspLeuGlnVal 246
Db 652 GTCACTGGCGTGTCTGCGCGATACGCAACACGCGATACATCGACTCGACGTT 711
Qy 247 SerGlyPhePheAlaIleGlyHisGluProAlaThrLysPheLeuGlyGlyGlnLeu 266
Db 712 CGCGGTCTGTTGTGCTATCGGTCAACGCGCAATACCTACTGCGATTTTCGAAGGCGCAGCTG 771
Qy 267 GluLeuAspSerAspGlyTyValGluThrLysProGly-----SerThrHis 282
Db 772 GAACGTGAA---AACGGCTACATCAAGTACATCGCTGGGTATTCATGGTAATGCCACCCAG 828
Qy 283 ThrSerValLysGlyValPheAlaAlaGlyAspValGlnAspLysLysTyTrpArgGlnAla 302
Db 829 ACCAGCATTCCTGGCGTCTTTGCGCGACGCGACGATGATGATCATATTATCGCCAGGCC 888
Qy 303 IleThrAlaAlaGlySerGlyCysMetAlaAlaLeuAspAlaGluHisTyIleu 320
Db 889 ATTACTTCGCGCGTACAGGCTGATGCGACGACTTGATGCGGAACGCTACCTC 942

```

RESULT 15

```

US-03-328-352-3988
; Sequence 3988, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04

```

```

; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 3988
; LENGTH: 954
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-3988

Alignment Scores:
Pred. No.: 6,48e-75 Length: 954
Score: 703.50 Matches: 144
Percent Similarity: 64.38% Conservative: 62
Best Local Similarity: 45.00% Mismatches: 97
Query Match: 41.16% Indels: 17
DB: 4 Gaps: 6

US-10-005-429-25 (1-331) x US-09-328-352-3988 (1-954)

Qy 11 ThrArgIleCysIleIleGlySerGlyProAlaAlaHisThrAlaAlaIleTyAlaAla 30
Db 16 TCACGCTCTGATAATCTCTGGTTCGCGCTTATAGTCGCGGCTATAGTCGAGCATATATGCGAGC 75
Qy 31 ArgAlaGluLeuLysProValLeuPheGluGlyTrpMetAlaAsnAspIleAlaAlaGly 50
Db 76 CGTCAAACTTAAACCTTCTTAATTCAGGT-----TTACAGCTTGGC 120
Qy 51 GlyGlnLeuThrThrThrAspValGluAsnPheProGlyPheProAsnGlyIleMet 70
Db 121 GGCACACTTCAACACACACGAGTTGACAACTGGCGCGGCTCTCTGAAGTTTAAACA 180
Qy 71 GlyAlaAspLeuMetAspAsnCysArgAlaGlnSerLeuArgPheGlyThrAsnIleLeu 90
Db 181 GGTCTGCTAATGAGTTCGTATGCAAGCAGCATGCTGAAGCTTGGTACAGAACTCGTC 240
Qy 91 SerGluThrValThrAlaValAspPheSerAlaCysProPheArgValSerAlaAspSer 110
Db 241 TATGACCATATTAACGAGTGGACTTAAATGATGCTGCTCTTCGTTCTTAAAGGTGATATG 300
Qy 111 ThrThrValLeuAlaAspAlaValIleValAlaThrGlyAlaValAlaAlaArgArgLeuHis 130
Db 301 GAAGAGTACATGATGATGCTTGTATGCAACTGGTCTGACGCTGATATCTTATCTGGC 360
Qy 131 PheProGlySerAspAlaTyTrpAsnArgGlyIleSerAlaCysAlaValCysAspGly 150
Db 361 CTACAGTCTGAACAAACTTTATGGGCAAGCGCTATGTCACACATGTGATGGT 420
Qy 151 AlaAlaProIlePheArgAsnLysProIleAlaValIleGlyGlyGlyAspSerAlaMet 170
Db 421 TTC-----TTCACAAAAACCAAAAGTAATGCTGTAGTGGTGTAACTGCTGTT 474
Qy 171 GluGlnSerAsnPheLeuThrLysTyTrpGlySerHisValTyIleIleHisArgArgAsn 190
Db 475 GAAGAGCATCTTATTTATCAATATTCCTTCATGCTAAGCTAGTACACCGCGGTGAT 534
Qy 191 ThrPheArgAlaSerLysIleMetGlnAlaArgAlaLeu-----GluAsnProLys 207
Db 535 AGCTTAGCTTCTGAAAAAGATTTTCAAGATCATTTATTTGTCAAAAGAAAAAGAGGAAA 594
Qy 208 IleLysValLeuTrpAspSerGluValGluAlaTyTrpGlyGlyAlaAsnGlyGlyPro 227
Db 595 ATCAGCATTATCTGGAATCAGAACTTGAAGAGTATGAGTGGTGGTGCACATCTGTT----- 648
Qy 228 LeuAlaGlyValLysValLysAsnLeuLeuAsnGlyGluValSerAspLeuGlnValSer 247
Db 649 GTAACAAGTGTTCGCTTAAATCAATCAAGATGAATCAAGCAAGACGCTAGAGGTTCAT 708
Qy 248 ThrLeuPhePheAlaIleGlyHisGluProAlaThrLysPheLeuGlyGlyGlnGlu 267
Db 709 GGTCTATCTGTTGCAATGCTGCTCAAAACCAAACTCTGGTATGTTGATGGTCAATTAAC 768
Qy 268 LeuAspSerAspGlyTyValGluThrLysProGly-----SerThrHisThr 283
Db 769 TTA---CGTGTGCTATATCCAGTACAAAGCGGTACTTCTGTAATGCAACGCAAC 825

```


PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/AU98/01023
 FILING DATE: 10-DEC-1998
 ATTORNEY/AGENT INFORMATION:
 NAME: Monroy, Gladys H
 REGISTRATION NUMBER: 32,430
 REFERENCE/DOCKET NUMBER: 27340-20021.00
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650-813-5600
 TELEFAX: 650-494-0792
 TELEX: 706141
 INFORMATION FOR SEQ ID NO: 685:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1443 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: circular
 MOLECULE TYPE: DNA (genomic)
 HYPOTHEICAL: NO
 ANTI-SENSE: UNKNOWN
 ORIGINAL SOURCE:
 ORGANISM: PORPHYROMONAS GINGIVALIS
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: 1...1443
 US-09-221-017B-685

Alignment Scores:
 Pred. No.: 2,22e-79 Length: 1443
 Score: 743.00 Matches: 156
 Percent Similarity: 62.97% Conservative: 43
 Best Local Similarity: 49.37% Mismatches: 105
 Query Match: 43.48% Indels: 12
 DB: 4 Gaps: 5

US-10-005-429-25 (1-331) X US-09-221-017B-685 (1-1443)

Qy 12 ArgLeuGlySerGlyProAlaAlaHisThrAlaAlaIleValAlaAlaArg 31
 Db 1189 CGCTGCTCATCATCGGTTCCGGAGCTCCGGCTATACCGGATATATGCTTCTCGT 1130
 Qy 32 AlaGluLeuLysProValLeuPheGluGlyTrpMetAlaAspIleAlaAlaGly 51
 Db 1129 GCCAACTCAACCCATCTCTACGAGG -----ATCAACCCGGCGGT 1085
 Qy 52 GlnLeuThrThrThrThrAspValGluAsnPheProGlyPheProAsnGlyLeuMetGly 71
 Db 1084 CAGCTAACGACTACGACCGAGGTGGAAGCTTCCCGGTTATCCCGAAGGAATCACCGGT 1025
 Qy 72 AlaAspLeuMetAspAsnGlyAlaGlnSerLeuArgPheGlyThrAsnIleLeuSer 91
 Db 1024 ACGGAACGATGGAAGACCTGCGCAACAGCAACCGCTTCGGAGCGGACATTCGTCG 965
 Qy 92 GluThrValThrAlaValAspPheSerAlaCysProPheArgValSerAlaAsp---Ser 110
 Db 964 GGTATCGCTACAAAGCGGATTTGAGCAAGGCTCTTACAGGATCACGATAGACGGAGAA 905
 Qy 111 ThrThrValLeuAlaAspAlaValIleValAlaThrGlyAlaValAlaArgLeuHis 130
 Db 904 AAGGAATACAGCGGATGCTTATCTCCAGGCTGCGCAACAGCAACCGCTTCGGAGCGGACATTCGTCG 845
 Qy 131 PheProGlySerAspAlaValTrpAsnArgGlyIleSerAlaCysAlaValCysAspGly 150
 Db 844 TTGGCGGATGAGCCAAATATCCCGCATGGGTCTTCTGTTGCTACCTGTGATGGA 785
 Qy 151 AlaAlaProIlePheArgAsnLysProIleAlaValIleGlyGlyAspSerAlaMet 170
 Db 784 TTT-----TTCTATCGCAAGGAAGAAAGTAGCCGTAGTGGGCGGAGGTACTGCTTGC 731
 Qy 171 GluGluSerAspPheLeuThrLysTrpGlySerHisValTrpIleIleHisArgAsn 190
 Db 730 GAGGAGGCTCTCTATCTGGCATCGCTGGCTGACAGCTGTACTGTATGCTACGCAAGAAC 671

Qy 191 ThrPheArgAlaSerLysIleMetGlnAlaArgAlaLeuGluAsnProLysIleLysVal 210
 Db 670 TATCTCGCTCCCAAGGTAAATGACAGGAGCGTGTATGAATACGCGCAACATAACCGTT 611
 Qy 211 LeuTrpAspSerGluValValGluAlaValGly-----GlyAlaAsnGlyGlyProLeu 228
 Db 610 CTCTTGAACATAATATACCGTGGGTCTATTTCGGGAAACGGTGTGAAGGTGCTCATCTG 551
 Qy 229 AlaGlyValLysValLysAsnLeuLeuAsnGlyGluValSerAspLeuGlnValSerGly 248
 Db 550 -----GTGAACCGCAAGAGAGCGGACGAGAGAGATGCTGCATCTGATGCT 497
 Qy 249 LeuPhePheAlaIleGlyHisGluProAlaThrLysPheLeuGlyGlyGlnLeuGluLeu 268
 Db 496 TTTTTCCTCGCTATCGTATACCGCAAACTCCGAAGATCTTCGCCGACCTACCTCGACTG 437
 Qy 269 AspSerAspGlyTrpValGluThrLysProGlySerThrHisThrSerValLysGlyVal 288
 Db 436 GACGAAGTGGTTATATCTTCGCGAAGGTTCTGTCGCCGCGCACAAAGTTCCCGCGCTA 377
 Qy 289 PheAlaAlaGlyAspValGlnAspLysLysTrpArgGlnAlaIleThrAlaAlaGlySer 308
 Db 376 TTTGCTCGCGGACGTTGCGGACCCACACTATCGTACGCTATCACGGCTGCGCGATCA 317
 Qy 309 GlyCysMetAlaAlaLeuAspAlaGluHisTrpLeuGlnGluIleGly 324
 Db 316 GGTTCGAAGCTCTATCTGAGAGCAGAGCGTTATTTCGGCGGACGCGT 269

RESULT 11
 US-09-328-352-1552
 ; Sequence 1552, Application US/09328352
 ; Patent No. 5562958
 ; GENERAL INFORMATION:
 ; APPLICANT: Gary L. Breton et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
 ; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: GTC99-03PA
 ; CURRENT APPLICATION NUMBER: US/09/328,352
 ; CURRENT FILING DATE: 1999-06-04
 ; NUMBER OF SEQ ID NOS: 8252
 ; SEQ ID NO 1552
 ; LENGTH: 963
 ; TYPE: DNA
 ; ORGANISM: Acinetobacter baumannii
 US-09-328-352-1552

Alignment Scores:
 Pred. No.: 5.44e-76 Length: 963
 Score: 712.50 Matches: 247
 Percent Similarity: 64.49% Conservative: 60
 Best Local Similarity: 45.79% Mismatches: 95
 Query Match: 41.69% Indels: 19
 DB: 4 Gaps: 7

US-10-005-429-25 (1-331) X US-09-328-352-1552 (1-963)

Qy 11 ThrArgLeuCysIleIleGlySerGlyProAlaAlaHisThrAlaAlaIleValAlaAla 30
 Db 31 TCTCGGTTAATATTCTCGGTTCTGCGGCTTATAGTGCAGCTGTTTATGCGAGCA 90
 Qy 31 ArgAlaGluLeuLysProValLeuPheGluGlyTrpMetAlaAsnAspIleAlaAlaGly 50
 Db 91 CGTCAATCTTAACCAACACACACTTATTGCGAGT-----TTACAGCTTGGC 135
 Qy 51 GlyGlnLeuThrThrThrThrAspValGluAsnPheProGlyPheProAsnGlyIleMet 70
 Db 136 GGCCCACTTACACACACACACCGAAGTTGACAACTGGCGGCGGATCTTGAAGTTTGACT 195
 Qy 71 GlyAlaAspLeuMetAspAsnGlyAlaGlnSerLeuArgPheGlyThrAsnIleLeu 90
 Db 196 GGTCTCGCTTAAATGAGCCGTTATCGAAGCATCATCGTTCGAGTGGTACCAACTTGTGTC 255
 Qy 91 SerGluThrValThrAlaValAspPheSerAlaCysProPheArgValSerAlaAspSer 110

QY 285 llysglyValPheAlaAlaGlyAspValGlnAspLysTyrArgGlnAlaIleThrAl 305
 Db 4394800 GCGGCGGCGTTCGCTCGCGGACCTGCTGATCGCATCTATCGCCAGCGGTACCGC 4394859
 QY 305 alaGlySerGlyCysMetAlaAlaLeuAspAlaGlnHisTyrLeuGlnGluIleGlyAl 325
 Db 4394860 AGCGGCGAGTGTGCTCGCGCGCTATCGACCGCGAGCGCTGCTCGCCGAG---CACGC 4394916

QY 325 aGlnGluGlyLysSerAsp 331
 Db 4394917 AGCAACCGGAGAGCTGAC 4394935

RESULT 9
 US-09-103-840A-1
 ; Sequence 1, Application US/09103840A
 ; Patent No. 6294328
 ; GENERAL INFORMATION:
 ; APPLICANT: FLEISCHMAN, Robert D.
 ; APPLICANT: WHITE, Owen R.
 ; APPLICANT: FRASER, Claire M.
 ; APPLICANT: VENTER, John C.
 ; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
 ; TITLE OF INVENTION: TUBERCULOSIS
 ; FILE REFERENCE: 24366-20007.00
 ; CURRENT APPLICATION NUMBER: US/09/103,840A
 ; CURRENT FILING DATE: 1998-06-24
 ; NUMBER OF SEQ ID NOS: 2
 ; SOFTWARE: Patent In Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 4411529
 ; TYPE: DNA
 ; ORGANISM: Mycobacterium tuberculosis
 ; OTHER INFORMATION: H37Rv
 US-09-103-840A-1

Alignment Scores:
 Pred. No.: 2,598-74 Length: 4411529
 Score: 747.00 Matches: 164
 Percent Similarity: 66.36% Conservative: 53
 Best Local Similarity: 50.15% Mismatches: 95
 Query Match: 43.71% Indels: 15
 DB: 3 Gaps: 6

US-10-005-429-25 (1-331) x US-09-103-840A-1 (1-4411529)

QY 8 ProLeuArgThrArg-IleCysIleIleGlySerGlyProAlaAlaHisThrAlaIle 27
 Db 4401757 CCACCGCGTTCGCGAGCGTATCGTATCGCTCGGTCGCGGCGGTACACTCGCGGCT 4401816
 QY 27 eTyrAlaAlaArgAlaGluLeuLysProValLeuPheGluGlyTyrMetAlaAsnAspIle 47
 Db 4401817 CTACGCGCGCGTGCACGCTGGCGCGCTGGTCTTCGAGGCG---AC 4401861
 QY 47 eAlaAlaGlyGlyGlnLeuThrThrThrThrThrThrThrThrThrThrThrThrThr 67
 Db 4401862 GTCTTCGCGCGCGCGTGTATGATACCCACCGAGCGTGGAGAACTTACCGCGGATTCGCAA 4401921
 QY 67 nGlyIleMetGlyAlaAlaAspLeuMetAspAsnCysArgAlaGlnSerLeuArgPheGlyTh 87
 Db 4401922 CGGCTACCGCGTTCAGATGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 4401981
 QY 87 rAsnIleLeuSerGluThrValThrAlaValAspPheSerAlaCysProPheArg----- 105
 Db 4401982 GGACCTCGTATGAGAGCGTGGAGTGGTATCATCTACCGGG---CCGCTGAAATCGGT 4402038
 QY 106 -ValSerAlaAspSerThrThrValLeuAlaAspAlaValIleValAlaThrGlyAlaVa 125
 Db 4402039 CGTCACCGCGCGAGCAGACACCCCGCGCGCGCGTGTATCTGCAATGGCGGAGC 4402098
 QY 125 lAlaArgLeuHisPheProGlySerAspAlaTyrTrpAsnArgGlyIleSerAlaCy 145
 Db 4402099 GGACAGCTATCTGACGTTGCGCGCGAGACAGGAATTCGTCGCGCGCGGTGAGCTCGTG 4402158

QY 145 sAlaValCysAspGlyAlaAlaPheArgAsnLysProIleAlaValIleGlyG1 165
 Db 4402159 GCGCACCTGCGACGAGTTC-----FTCTTCGCGATCAGGACATCGCGCGTATCGGCGG 4402212
 QY 165 yGlyAspSerAlaMetGluGluSerAsnPheLeuThrLysTyrGlySerHisValTyrI1 185
 Db 4402213 CGGTGACTCGGCATATGAGGAGTACCTTCTGACCGGATTCGCTCGCAGTGTGACGCT 4402272
 QY 185 eIleHisArgArgAsnThrPheArgAlaSerLysIleMetGlnAlaArgAlaLeuGluAs 205
 Db 4402273 GGTGATCGCGCGACGAGTTCGCGGCTTCCAAATATCATGTCGATCGCGCGCGCAACAA 4402332
 QY 205 nProLysIleLysValLeuTrpAspSerGluValValGluAlaTyrGlyGlyAlaAsnG1 225
 Db 4402333 CGACAGATACGTTCTTCACCAACACACCGTGTTCGCGTGGACGCGGACACCA-- 4402390
 QY 225 yGlyProLeuAlaGlyValLysValLysValLysValLysValLysValLysValLys 245
 Db 4402391 -----GTGACCGGCTTTCGCGGTACGCGACACCAACACCGTTCGCGGACACCA 4402443
 QY 245 nValSerGlyLeuPheAlaIleGlyHisGluProAlaThrLysPheLeuGlyGlyG1 265
 Db 4402444 GGTAAACCGGTTTTCGTCGCGATCGCGCACGCGCGGTTCGCGTGGTGGTGGTGGTGGTGG 4402503
 QY 265 nLeuGluLeuAspSerAspGlyTyrValGluThrLysProGlySerThrHisThrSerVa 285
 Db 4402504 CATCGACGTCGACCGGACGCGCTACGTGTGTCGAGCGGCGTACCAACGACGACCTCACT 4402563
 QY 285 lLysGlyValPheAlaAlaGlyAspValGlnAspLysTyrArgGlnAlaIleThrAl 305
 Db 4402564 GCGCGCGGTTCGCTCGCGGCGACCTGCTGATCGCGGCGCTATCGCGAGCGGTATCGCG 4402623
 QY 305 aAlaGlySerGlyCysMetAlaAlaLeuAspAlaGluHisTyrLeuGlnGluIleGlyAl 325
 Db 4402624 AGCGGCGAGTGTGTCGCGCGCGCTATCGACCGCGCGGCTGCTGCGCGGCTGCGCGAG--CACGC 4402680

RESULT 10
 US-09-221-017B-685/c
 ; Sequence 685, Application US/09221017B
 ; Patent No. 6444799
 ; GENERAL INFORMATION:
 ; APPLICANT: Ross, Bruce C.
 ; TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
 ; NUMBER OF SEQUENCES: 1120
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSES: MORRISON & FOERSTER
 ; STREET: 755 PAGE MILL ROAD
 ; CITY: Palo Alto
 ; STATE: Ca
 ; COUNTRY: USA
 ; ZIP: 94304-1018
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: Windows
 ; SOFTWARE: FastSeq for Windows Version 2.0b
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/221,017B
 ; FILING DATE: 23-DEC-1998
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PP1182
 ; FILING DATE: 31-DEC-1997
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PP1546
 ; FILING DATE: 30-JAN-1998
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PP2911
 ; FILING DATE: 09-APR-1998

Db 463 TCCAGCTTACCTCTCTCCCGCCCTTCAAGATGTGGACCGAGTGGACGATGACGAA 522
Qy 108 AlaaspSerThrThrValLeuAlaaspAlaValleValalathrGlyAlaValAlaArg 127
Db 523 GGCAGCGAGCGCGTCCGCGACCGCGCGCGTCAATTCATTCACAGCGCGCAACCGCGCG 582
Qy 128 ArgLeuHisPheProGlySerAspAlaTyrTrpAsnArgGlyLeuSerAlaCysAlaVal 147
Db 583 CGTCTGACCTGCGCGCGAGGAGCACTTCTGGCAGAACGGAATCAGCGCTGTGCGTC 642
Qy 148 CysaspGlyAlaAlaProfilePheArgAsnLysProLeuAlaValleGlyGlyGlyAsp 167
Db 643 TGCAGCGTGCCTTCCGTAACCAAGCCCTGTACGTCATTCGCGGTGTGTCAC 702
Qy 168 SerAlaMetGluGluSerAsnPheLeuThrLysTyrGlySerHisValTyrLeuHis 187
Db 703 TCCGCGCCCGAGGAGGCGATCTTCTGCGCAAGTACCGCAGCGTACTGTCTCTGTT 762
Qy 188 ArgArgAsnThrPheArgAlaSerLysLeuMetGlnAlaArgAlaLeuGluAsnProLys 207
Db 763 CGCAAGGACAGCTGCGCTCTTCAACACCGCTCTTCAACATCATGCTGATCTCTCTCC 822
Qy 208 IleLysValLeuTrpAspSerGluValAlaGluAlaTyrGlyGlyAlaAsnGlyGly 226
Db 823 TGCAGGTCGCGCTTCAACACCGCTGCGCACCAGGTTATCGCGAGAACCAAGCTTAACGGC 882
Qy 227 ProLeuAlaGlyValLysValLysAsnLeuLeuAsnGlyGluValSerAspLeuGlnVal 246
Db 883 CTCATGACCCACCTCGGTGTCAGGACGTTCTCTTAACGCGGAGGAGTCTGTGAGGCT 942
Qy 247 SerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLysPheLeuGlyGlyGlnLeu 266
Db 943 AACGGTCTCTTCTAGCTGTGTGTCAGACCGCCCGCAGTGTCTCTGTCACAGGGCCAGGTT 1002
Qy 267 GluLeuAspSerAspGlyTyrValGluThrLysProGlySerHisThrSerValLys 286
Db 1003 GAGCTCGACGACGAGGATATCATCATCAACGCGCGGTACTAGCTTCACTAAGTCGAG 1062
Qy 287 GlyValPheAlaAlaGlyAspValGlnAspLysTyrArgGlnAlaIleThrAlaAla 306
Db 1063 GGTGTTTTCGCTGCGGTGATGTTCAGGATTAAGCGCTACCGTCAAGGCTATCACCAGTGC- 1121
Qy 306 ----- 306
Db 1122 CGGTATGTTCATCTTCAAGATCTCATTCATGTAATTCGAATTTGGTAACTCAATATT 1181
Qy 307 -----GlySerGlyCysMetAlaAlaLeuAspAlaGluHisTyrLeuGlnGluIleGly 324
Db 1182 CTACAGGATCTGCTGTGTCGCTGCTCTTGAGGCTGAGAAATTCATCGCGAGACCGAG 1241
Qy 325 Ala---GlnGluGlyLys 329
Db 1242 ACTCACCAGGAGGCAAG 1259
RESULT 8
US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA

; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
Alignment Scores:
Prob. No.: 2,59e-74 Length: 4403765
Score: 747.00 Matches: 164
Percent Similarity: 66.36% Conservative: 53
Best Local Similarity: 50.15% Mismatches: 95
Query Match: 43.71% Indels: 15
DB: 3 Gaps: 6
US-10-005-429-25 (1-331) x US-09-103-840A-2 (1-4403765)
Qy 8 ProLeuArgThrArg-IleCysIleIleGlySerGlyProAlaAlaAlaHisThrAlaAla 27
Db 4393993 CCACCCGCTGCGCGAGTATCGTTCATCGCTCCCGCGGGGTACTCTCGCGGCT 4394052
Qy 27 eTyrAlaAlaArgAlaGluLeuLysProValLeuPheGluGlyTyrMetAlaAsnAsp 47
Db 4394053 CTAAAGCGCGCGCTGCGCGAGTGGCGCGCTGCTTTCGAGGGC-----AC 4394097
Qy 47 eAlaAlaGlyGlyGlnLeuThrThrThrAspValGluAsnPheProGlyPheProAs 67
Db 4394098 GTCTTTTCCGCGCGCGCTGATGACACCGACGCGTGGAGAACTACCGCGGATTTCCCAA 4394157
Qy 67 nGlyIleMetGlyAlaAspLeuMetAspAsnCysArgAlaGlnSerLeuArgPheGly 87
Db 4394158 CGGATCATCCGCTCCAGAGTTGATGTAGATGCGCGGAGAACGCGCTGCGATTCGCGC 4394217
Qy 87 rAsnIleLeuSerGluThrValThrAlaValAspPheSerAlaCysProPheArg----- 105
Db 4394218 GGACCTGCGTATGGAAGACGTCGAGTCGCTATCATCTTCACGGG---CCGCTGAAATCGGT 4394274
Qy 106 -ValSerAlaAspSerThrThrValLeuAlaAspAlaValleValAlaThrGlyAla 125
Db 4394275 CGTACCGCGCGAGCGACAGACCCCGCGCGCGAGCGGATCTGCGCATGCGCGCAGC 4394334
Qy 125 lAlaArgAlaGluHisPheProGlySerAspAlaTyrTrpAsnArgGlyLysSerAla 145
Db 4394335 GGCACGCTATCTCAGCGTCCCGCGCAACAGGAATTTGTCGCGCGCGGGGTGAGTCGTG 4394394
Qy 145 sAlaValCysAspGlyAlaAlaProIlePheArgAsnLysProIleAlaValleGly 165
Db 4394395 CGCCACCTCGCAGCGGATTC-----TTCCTCCGATCAGGACATCCCGCTCATCGCGG 4394448
Qy 165 yGlyAspSerAlaMetGluGluSerAsnPheLeuThrLysTyrGlySerHisValTyr 185
Db 4394449 CGGTGCTCGCATATGGAAGAGCTACCTTCTGACCGGATTCGTCGCGAGTGTGAGCT 4394508
Qy 185 eIleHisArgAsnThrPheArgAlaSerLysIleMetGlnAlaArgAlaLeuGluAs 205
Db 4394509 GGTGCTATCGCGCGAGTTCGCGGCTTCCAAATCATGCTCGATCGCGCGCGCAACAA 4394568
Qy 205 nProLysIleLysValLeuTrpAspSerGluValAlaGluAlaTyrGlyAlaAsnG 225
Db 4394569 CGACAGATACGTTCTCTACCAACACACCGCTGCTGCGCGGAGCACCCACA-- 4394626
Qy 225 yGlyProLeuAlaGlyValLysValLysAsnLeuLeuAsnGlyGluValSerAspLeu 245
Db 4394627 -----GTGACCGCGCTGCGGCTGCGGACACCAACCGCTGCGGAAACCCCTGCC 4394679
Qy 245 nValSerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLysPheLeuGlyGly 265
Db 4394680 GGTAACCGGTGTTTTCGTCGATCGGCGACAGCGCGTCTGGGCTTGGTGGCGGAGGC 4394739
Qy 265 nLeuGluLeuAspSerAspGlyTyrValGluThrLysProGlySerHisThrSerVa 285
Db 4394740 CATCGACGTGCAACCGCGCGCTACGTGCTGCTGCGAGGCGGTACCAACGACCTCACT 4394799

Qy	167	AppSerAlaMetGluGluSerAsnPheLeuThrLysTyrGlySerHisValTyrIleLeu	186
Db	366122	GAATCTCGTTTTAGAGAAGAGCTCTTTACCTGACTCGTATGGAAGCCACGATATATGAGTT	366063
Qy	187	HisArgArgAsnThrPheArgAlaSerLysIleMetGlnAlaArgAlaLeuGluAsnPro	206
Db	366062	CATCGTAGAGATAACTCGGGGCTTCTAAAGCTATGGAAGCTCGGGCGCAACATGAA	366003
Qy	207	LysIleLysValLeuTyrAspSerGluValValGluAlaTyrGlyGlyAlaAsnGlyGly	236
Db	366002	AAAATTACATTTTATGCAATAGCAGAGTTGTAAAAAATTTCTCGACATAGC-----	365952
Qy	227	ProLeuAlaGlyValLysValLysValLysValLysValLysValLysValLysVal	246
Db	365951	ATTCTCGCTCCGTAGATATTAGAAATGTTACAGACTCAAGAAATTTACAACTAGAGAAGCT	365892
Qy	247	SerGlyLeuPhePheAlaIleGlyHisGluProAlaLaThrLysPheLeuGlyGlyGlnLeu	266
Db	365891	CGCGGGGTGTTCTTTGCTATAGCCATAGCCCAATAACGATTTTCTCGAGGACAGCTG	365832
Qy	267	GluLeuAspSerAspGlyTyrValGluThrLysProGlySerThrHisThrSerValLys	286
Db	365831	ACGTTAGATGAGTCGGGCTATTTGTGACTGAGAAGGAACGTCGAAGACTTCTGTCCT	365772
Qy	287	GlyValPheAlaAlaGlyAspValGlnAspLysLysTyrArgGlnAlaIleThrAlaAla	306
Db	365771	GGAGTATTGCTGCTGGAGATGTTCCAGATAAGTACTATCGTCAGGCGGTACTTCTGCA	365712
Qy	307	GlySerGlyCysMetAlaAlaLeuAspAlaGluHisTyrLeu	320
Db	365711	GGAGTGGTGTGATAGCAGCACTAGATGCTGAAGATTCTTA	365670

RESULT 7

US-08-386-729A-6

Sequence 6, Application US/08386729A

Patent No. 5753435

GENERAL INFORMATION:

APPLICANT: Aharonowitz, Yair

APPLICANT: Van Der Voort, Lucia H. M.

APPLICANT: Cohen, Gerald

APPLICANT: Bovenberg, Roelof A. L.

APPLICANT: Schreiber, Rachel

APPLICANT: Argaman, Anat

APPLICANT: Av-Gay, Yosef

APPLICANT: Nan, Helena M.

APPLICANT: Kattavilder, Alfred

APPLICANT: Pallissa, Harriet

TITLE OF INVENTION: An oxido reductase enzyme system

TITLE OF INVENTION: obtainable from P. chrysogenum, the set of genes

TITLE OF INVENTION: encoding the same and the use of oxido reductase enzyme

TITLE OF INVENTION: systems or genes encoding the same for increasing antibiotic

TITLE OF INVENTION: production

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: Weil, Gotehal & Manges

STREET: 2882 Sand Hill Road, Ste. 280

CITY: Menlo Park

STATE: CA

COUNTRY: U.S.A.

ZIP: 94025

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" diskette

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/386,729A

FILING DATE: 10-FEB-1995

CLASSIFICATION: 435

PRIOR APPLICATION NUMBER:

APPLICATION NUMBER: US 08/274,043

FILING DATE: 12-JULY-1994

APPLICATION NUMBER: US 07/820,688


```
Db 322 AAGCCATTCGCTGACGCTGATTCGCTATCGGAGCTGTGCTAAGTGGCTTACG 381
Qy 131 PheProGlySer-----AspAlaTyTrpAsnArgGlyIleSerAlaCysAla 146
Db 382 TTCGTTGGATCTGGTCAAGTTCGCGAGGTTTGTGGAACCGTGGATCTCCGCTTGTGT 441
Qy 147 ValCysAspGlyAlaAlaProIlePheArgAsnLysProIleAlaValIleGlyGly 166
Db 442 GTTTCGCGAGGAGCTCTCCGATATTCGCAACAACTTCGCGGTGATCGGTGGAGC 501
Qy 167 AspSerAlaMetGluGluSerAsnPheLeuThrLysTy-GlySerHisValTyIleIle 186
Db 502 GATTCGCAATGGAAGAGCAACTTCTTCAAAATATGGATCTAAAGTGATATAATC 561
Qy 187 HisArgArgAsnThrPheArgAlaSerLysIleMetGlnAlaArgAlaLeuGluAsnPro 206
Db 562 GATAGCAGAGATCTTTTATAGAGGCTCTAAGATTATGCGAGCGACT-TGTCTAATCCT 620
Qy 207 LysIleLysValLeuTrpAspSerGluValGluAlaTyGlyGlyAlaAsnGlyGly 226
Db 621 AAGATTGATGTGATTGTGGAAGCTCTGCTGTGTGGAGCTTATGGAGATGGAGAAAGAT 680
Qy 227 ProLeuAlaGlyValLysValLysAsnLeuLeuAsnGlyGluValSerAspLeuGlnVal 246
Db 681 GTGCTTGGAGGATTGAAGTGAAGATGTGTTACCGGAGATGTTTCTGATTTAAAGTT 740
Qy 247 SerGlyLeuPhePheAlaIleGlyHisGluProAlaThrTyPheLeuGlyGlnLeu 266
Db 741 TCTGGATTGTTCTTCTGCTATGTGTCATGAGCCAGCTACCAAGTTTGTGATGTTGT 800
Qy 267 GluLeuAspSerAspGlyTyValGluThrLysProGlySerThrHisThrSerValLys 286
Db 801 GAGTTAGATTGGATGTTATGTTGTACGAGAGCTTGTACTACAGACTAGCGTTCC 860
Qy 287 GlyValPheAlaAlaGlyAspValGlnAspLysTyTrpArgGlnAlaIleThrAlaAla 306
Db 861 CGAGTTTTCGCTCGCGGTGATGTTTCAGGATAGAGATATAGGCAAGCCATCACTGCTGCA 920
Qy 307 GlySerGlyCysMetAlaAlaLeuAspAlaGluHisTyLeuGlnGluIleGlyAlaGln 326
Db 921 GGAACGCGGTGCATGCGAGCTTGGATGAGAGCATTAATTACAGAGATTGGATCTCAG 980
Qy 327 GluGlyLysSerAsp 331
Db 981 CAAAGTAAGATGAT 995

RESULT 6
US-09-198-452A-1/c
; Sequence 1, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffiths, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 1
; LENGTH: 1230025
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1..(15000))
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc feature
; LOCATION: (15001..(30000))
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc feature
; LOCATION: (30001..(45000))
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc feature
; LOCATION: (45001..(45000))
; OTHER INFORMATION: n=a or c or g or t

; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc feature
; LOCATION: (45001..(60000))
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc feature
; LOCATION: (60001..(75000))
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc feature
; LOCATION: (75001..(90000))
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc feature
; LOCATION: (90001..(105000))
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc feature
; LOCATION: (105001..(120000))
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc feature
; LOCATION: (120001..(135000))
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc feature
; LOCATION: (135001..(150000))
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc feature
; LOCATION: (150001..(165000))
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc feature
; LOCATION: (165001..(180000))
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc feature
; LOCATION: (180001..(195000))
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc feature
; LOCATION: (195001..(210000))
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc feature
; LOCATION: (210001..(225000))
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc feature
; LOCATION: (225001..(240000))
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc feature
; LOCATION: (240001..(255000))
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc feature
; LOCATION: (255001..(270000))
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc feature
; LOCATION: (270001..(285000))
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc feature
; LOCATION: (285001..(300000))
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc feature
; LOCATION: (300001..(315000))
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc feature
; LOCATION: (315001..(330000))
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc feature
; LOCATION: (330001..(345000))
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc feature
; LOCATION: (345001..(360000))
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc feature
; LOCATION: (360001..(375000))
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc feature
; LOCATION: (375001..(390000))
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc feature
; LOCATION: (390001..(405000))
; OTHER INFORMATION: n=a or c or g or t
```

```

; SEQ ID NO 24
; LENGTH: 1021
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-598-747-24

Alignment Scores:
Pred. No.: 2,18-145 Length: 1021
Score: 1290.00 Matches: 251
Percent Similarity: 85.54% Conservatives: 27
Best Local Similarity: 77.23% Mismatches: 43
Query Match: 75.48% Indels: 4
DB: 4 Gaps: 1

US-10-005-429-25 (1-331) x US-09-598-747-24 (1-1021)

Qy 11 ThrArgLeuGlySerGlyProAlaAlaHisThrAlaAlaLeuTyrAlaAla 30
Db 34 ACCGCGCTCTGATCGTTGGCTCGCGCGCTCCACACCGCGCATCTACGCGGCC 93
Qy 31 ArgAlaGluLeuLysProValLeuPheGluGlyTrpMetAlaAsnAspIleAlaAglly 50
Db 94 CGCCCGAGCTGAGCGCTCTCTTGGAGGCTGGATGGCCACGACATCGCCCGGCC 153
Qy 51 GlyGlnLeuThrThrThrAspValGluAsnPheProGlyPheProAsnGlyIleMet 70
Db 154 GGCAGCTCACACACACCGAGCTGAGAACTTCGCGGCTTCGCGGAGGGCATCTC 213
Qy 71 GlyAlaAspLeuMetAspAsnGlyArgAlaGlnSerLeuArgPheGlyThrAsnIleLeu 90
Db 214 GCGTGGAGCTGACCGCAAGTTCGCAAGCAGAGCGAGCGCTTCGCGACCACTTTC 273
Qy 91 SerGluThrValThrAlaValAspPheSerAlaCysProPheArgValSerAlaAspSer 110
Db 274 ACCGAGCCGTGACCAAGTGGACTTCTCGAGCAAGCGGTTCAAGCTCTTCACCGACTCC 333
Qy 111 ThrThrValLeuAlaAspAlaValIleValAlaThrGlyAlaValAlaArgGluHis 130
Db 334 AAGCCCATCTCGCGAGCGCGGTATCTCCGCAATCGCGCGCTGGCGCAAGTGGCTTCC 393
Qy 131 PheProGlySer-----AspAlaTyrTrpAsnArgGlyIleSerAlaCysAla 146
Db 394 TTCTGGGCTTCGCGAGGTCTCGCGCGCTCTGGAAACCGCGGCATCTCGCGTGGCT 453
Qy 147 ValCysAspGlyAlaAlaProIlePheArgAsnLysProIleAlaValIleGlyGly 166
Db 454 GTGTGCGAGCGCGCGCGCTCTTCGCGCAACAGCGGCTCGCTGTGATCGTGGCGGA 513
Qy 167 AspSerAlaMetGluGluSerAsnPheLeuThrLysTyrGlySerHisValTyrIleIle 186
Db 514 GACAGCGCGATGAGAGAGCGCAATCTCTCCAGTACGAGTCCAGGTGTATCATC 573
Qy 187 HisArgArgAsnThrPheArgAlaSerLysIleMetGlnAlaArgAlaLeuGluAsnPro 206
Db 574 GACGCGCGCGAGCGCTTCGCGCGCTTCCCAAGATCATGACGAGCGCGCGCTCTCCAACCG 633
Qy 207 LysIleLysValLeuTrpAsnSerGluValValGluAlaTyrGlyGlyAlaAsnGlyGly 226
Db 634 AAGATCGACGCTATCTCGAGTCTCTCGGTGGTGGAGGCTACGCGAGCGCGCGCGGAC 693
Qy 227 ProLeuAlaGlyValLysValLysAsnLeuLeuAsnGlyGluValSerAspLeuGlnVal 246
Db 694 GTGCTCGCGCGCTCAAGGTGAAGAACGTGTGTGACCGCGAGCGGTGTCCGACCTCAAGGTG 753
Qy 247 SerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLysPheLeuGlyGlyGlnLeu 266
Db 754 TCGCGCTCTCTTCGCGCATCGCGCACGAGCGCGCGCACCAAGTTCCTCGAGCGCGCGGTG 813
Qy 267 GluLeuAspSerAspGlyTyrValGluThrLysProGlySerThrHisThrSerValLys 286
Db 814 GAGCTGGACTCCGAGCGCTACGTGTGTACCAAGCGCGCGCACCCACGACCTCCGTGCT 873
Qy 287 GlyValPheAlaAlaGlyAspValGlnAspLysLysTyrArgGlnAlaIleThrAlaAla 306

```

```

RESULT 5
US-09-540-014-26
; Sequence 26, Application US/09540014
; Patent No. 6380372
; GENERAL INFORMATION:
; APPLICANT: Cho, Myeong-Je
; APPLICANT: Del'Val, Greg
; APPLICANT: Calliau, Maxime
; APPLICANT: Lemauz, Peggy G.
; APPLICANT: Buchanan, Bob B.
; TITLE OF INVENTION: Barley Gene for Thioresoxin and
; FILE REFERENCE: 2001-0701.30
; CURRENT APPLICATION NUMBER: US/09/540,014
; CURRENT FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 60/127,198
; PRIOR FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: US 60/169,162
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: US 60/177,740
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 60/177,739
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 998
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-540-014-26

```

```

Alignment Scores:
Pred. No.: 1,06e-136 Length: 998
Score: 1217.50 Matches: 244
Percent Similarity: 83.38% Conservatives: 27
Best Local Similarity: 75.08% Mismatches: 49
Query Match: 71.24% Indels: 6
DB: 4 Gaps: 2

```

US-10-005-429-25 (1-331) x US-09-540-014-26 (1-998)

```

Qy 11 ThrArgLeuGlySerGlyProAlaAlaHisThrAlaAlaLeuTyrAlaAla 30
Db 25 ACAAGGCTCTGTATCGTAGGAGTGGCCAGCGGCAACACGCGCGGATTTACGAGCT 84
Qy 31 ArgAlaGluLeuLysProValLeuPheGluGlyTrpMetAlaAsnAspIleAlaAglly 50
Db 85 AGGCTGAACCTTAACCTCTCTCTCGAAGGATGATGCTTAACGACATCGCTCCCGT 144
Qy 51 GlyGlnLeuThrThrThrAspValGluAsnPheProGlyPheProAsnGlyIleMet 70
Db 145 GGTCAACTCAACCAACACCGCGCT---GAGAAATTTCCCGGATTTCCAGAGGTATTCTC 201
Qy 71 GlyAlaAspLeuMetAspAsnGlyArgAlaGlnSerLeuArgPheGlyThrAsnIleLeu 90
Db 202 GGAGTAGAGTCACTGACAAATTCGTAACATCGGAGCGATTCGCTACTACGATATT 261
Qy 91 SerGluThrValThrAlaValAspPheSerAlaCysProPheArgValSerAlaAspSer 110
Db 262 ACAGAGCGGTGACGAAAGTGGATTTCTCTTCAAAACCGTTTAAGCTATTTCACAGATTCA 321
Qy 311 ThrThrValLeuAlaAspAlaValIleValAlaThrGlyAlaValAlaArgGluHis 130

```


Qy		161	AlaValIleGlyGlyGlyAspSerAlaMetGluSerAsnPheLeuThrLysTyrGly	180
Dd		481	GCGGTTCATCCGGCGGGCTGCATTCCGCCATGAGGAAGCCAACCTTCCTCACCAAGTAGCGGA	540
Qy		181	SerHisValTyrIleIleHisArgArgAsnThrPheArgAlaSerLysIleMetGlnAla	200
Dd		541	TCCCAAAGTGATCATCATCAACGGCGCAACACTTCGGCGCTCCAGATTATGCAAGCT	600
Qy		201	ArgAlaLeuGluAsnProLysIleLysValLeuTrpAspSerGluValValGluAlaTyr	220
Dd		601	AGGGCGCTCTCCAAATCCTTAAGATCCAGGTTCGTCTGGGACTC-GAGGTCTGTCGAGGCTTAC	659
Qy		221	GlyGlyAlaAsnGlyGlyProLeuAlaGlyValLysValllysAsnLeuLeuAsnGlyGlu	240
Dd		660	GACGGTCAGGGCGGGGCCCATAGCTGGGCTCAAGAACCTTGTTGACTGGTGGAG	719
Qy		241	ValSerAspLeuGlnValSerGlyLeuPhePheIleGlyHisGluProIlaThrLys	260
Dd		720	GTGTCGTGACTTCAGGTGTCGGGGCTTTCTTCGCCATCGGGCATGAGCCGGCCACAAG	779
Qy		261	PheLeuGlyGlyGlnLeuGluLeuAspSerAspGlyTyrValGluThrLysProGlySer	280
Dd		780	TTTTCTCAATGGGCGAGCTTGAGCTCCATCCCGATGGGTATGTGGCCACCAGCCGGGCTCT	839
Qy		281	ThrHisThrSerValLysGlyValPheAlaIleGlyAspValGlnAspLysLysTyrArg	300
Dd		840	ACACATACCAGTGTGA-GGGGTCTTTCTCTCTGGAGACGTGCACAGATAAAGAATPCGT	898
Qy		301	GlnAlaIleThrAlaAlaGlySerGlyCysMetAlaAlaLeu-AspAlaGluHisTyrIle	320
Dd		899	CAGGCCATTACTGCTGCTGGATCAGTTGCATGGCTGCTTTGGGACGCCGAGCACAATCT	958
Qy		320	uGlnGluIleGlyAlaGlnGluGlyLysSerAsp	331
Dd		959	GAGAGAGGTGGGTGCACAGGTGGGCAAGTCTGAT	992

RESIST 3

US-09-598-747-26

; Sequence 26, Application US/09598747

; Patent No. 6531648

GENERAL INFORMATION:

APPLICANT: Lananan, Michael B.

APPLICANT: Desai, Nalin M.

APPLICANT: Gascaska, Pamela I.
TITLE OF INVENTION: CRYSTAL PROCE

1. TITLE OF INVENTION: GRAIN PROCESSING METHOD AND INGENUOUS FEEDS USED THEREIN

TITLE OF INVENTION: THEFT
FILE REFERENCE: A-31383D7

FILE REFERENCE: R 315031
CURRENT APPLICATION NUMBER: US/09/598.747

CURRENT FILING DATE: 2000-06-21

NUMBER OF	SEO ID NOS-	42
-----------	-------------	----

SOFTWARE: PatentIn Ver. 2.1

: SEQ ID NO 26

; LENGTH: 1560

; TYPE: DNA

; ORGANISM: Oryza sativa

US-09-598-747-26

Alignment Scores:			
Pred. No.:	1,01e-167	Length:	1560
Score:	1478.00	Matches:	282
Percent Similarity:	96.13%	Conservative:	15
Best Local Similarity:	91.26%	Mismatches:	12
Query Match:	68.49%	Indels:	0
DB:	4	Gaps:	0

US-10-005-429-25 (1-331) x US-09-598-747-26 (1-1560)

Qy 1 MetGluGlySerAlaalaalaProLeuenaThrArgIleCysIleIleGlySerGlyPro 20
Db 406 ATGAGGGATCCCGGGGGCGCGCTCCGACAGCGCCTGTCATCATCGGAGCG3CCG 465
Qy 21 AlaAlaHisThrAlaalaIleTyrralalaArgAlaGluLeuLysProValLeuPheGlu 40

466	TCGGCGCACACGCGGGGAGTCTACGCGCGCGCGGAGCTCAAGCCCGGTGCTCTTCGAG	525
41	GlyTrpMetAlaAsnAspIleAlaAlaGlyGlyGlnLeuThrThrThrThrAspValGlu	60
526	GGTGGCTCGCCAAACACATCGCGGGGGGGCCAGCTCACCAACCAACCGCGTCTCGAG	585
61	AsnPheProGlyPheProAsnGlyIleMetGlyAlaAspLeuMetAspAsnCysArgAla	80
586	AACTTCCCGGGTTCCCGAAGGGGATCTCTCGCGGGGAGCTCATGTGTCGGTGC CGGCC	645
81	GlnSerLeuArgPheGlyThrAsnIleLeuSerGluThrValThrAlaValAspPheSer	100
646	CAGTCTCTCCGGTTCGCAACCAAGCATCATCTCGAGACCGTCAACCGCGTCTCTTCC	705
101	AlaCysProPheArgValSerAlaAspSerThrThrValLeuAlaAspAlaValIleVal	120
706	GGCGGCGCCCTTCGCGTCTCGCATCCACCATCGTCTCGCGCACCGCTCGTCGTC	765
121	AlaThrGlyAlaValAlaArgLeuHisPheProGlySerAspAlaThrTrpAsnArg	140
766	GCCACCGGGCGCGTCCGCGGGACTTCACTTCGCGGGCTCGACGCCCTACTCGAACCCG	825
141	GlyIleSerAlaCysAlaValCysAspGlyAlaAlaProIlePheArgAsnLysProIle	160
826	GGCATCTCAGCCTCGCGCGTCTGCGAGGGGGCGCCCAATCTTCAGGAACAACCCATC	885
161	AlaValIleGlyGlyAspSerAlaMetGluGluSerAsnPheLeuThrLysTyrGly	180
886	GCGCTCATCGCGCGCGCATCCGCGCATGGAGAGTCCAACCTCTCTCAACAAGTAGCGG	945
181	SerHisValTyrIleIleHisArgArgAsnThrPheArgAlaSerLysIleMetGlnAla	200
946	TCCCATGTGTACATCATCCACCGCGCCACACCTTCGCGCCCTCCAAGATCATGACGCC	1005
201	ArgAlaLeuGluAsnProLysIleLysValLeuTrpAspSerGlnValValGluAlaTyr	220
1006	AGGGCGTGTGCAAAACCCCAAGATCCAGGTTTTCTGGGACCTCGAGGTCGTGAGGCCCTAC	1065
221	GlyGlyAlaAsnGlyGlyProLeuAlaGlyValLysValLysAsnLeuLeuAsnGlyGlu	240
1066	GGCGGCGAGGTCGAGGTCCATTGGCTGGTGTCAAGGTGAAGAACTTGGTTACTTGGGAAG	1125
241	ValSerAspLeuGlnValSerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLys	260
1126	ATCTCGACGCTTCAGGTGTCGGGTCTCTTCCTCGCCATCGGACATGAACCGGCGAGAG	1185
261	PheLeuGlyGlyGlnLeuGluLeuAspSerAspGlyTyrValGluThrLysProGlySer	280
1186	TTTTCTCGCGGGCAGCTTCAGCTCGATGTGATGGGTATGTGGGCCCAACCAAGCCAGCTCC	1245
281	ThrHisThrSerValLysGlyValPheAlaAlaGlyAspValGlnAspLysLysTyrArg	300
1246	ACGCACACCATGTTGAAGGGGGTCTTTGCTGCTGGGGAGTGTGCGGACACAAGATTCGC	1305
301	GlnAlaIleThrAlaAlaGlySerGly	309
1306	CAGGCTATTACTCCGCTGGATCAGGT	1332

RESULT 4

US-09-598-747-24

; Sequence 24, Application US/09598747

; Patent No. 6531648

; GENERAL INFORMATION:

; APPLICANT: Lanahan, Michael B.

APPLICANT: Desai, Nalini M.

APPLICANT: Gasdaska, Pamela Y.

; TITLE OF INVENTION: GRAIN PRO-
; TECTANT
; TIME OF INVENTION: THIRTYN-

;; TITLE OF INVENTION: THERE
;; REFERENCE: 3,330,331

FILE REFERENCE: A-31383PI
CURRENT ADDICTION NUMBER: US/00/598 247

CURRENT AFFILIATION NUMBER: 03/0
CURRENT FILING DATE: 2000-06-21

;	CURRENT FINDING DATE:	200
:	NUMBER OF SEQ ID NOS-	42

: SOFTWARE: Patent In Ver. 2.1

Query Match: 88.36% Indels: 3
DB: 4 Gaps: 0

US-10-005-429-25 (1-331) x US-09-540-014-110 (1-995)

QY 1 MetGluGlySerAlaAlaAlaProLeuArgThrArgIleCysIleIleGlySerGlyPro 20
DB 1 ATGGAGGATCCGCGCGCGCGCGCTCCGACAGCGGTCGATCATCGGAGCGCGCG 60

QY 21 AlaAlaHisThrAlaAlaIleTyAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 40
DB 61 GCCGCGCACACGCGCGCGCTATCCGCGCGCGCGCGAGCTCAAGCGCGCTCTTCGAG 120

QY 41 GlyTyrMetAlaAsnAspIleAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 60
DB 121 GGCTGGATGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180

QY 61 AsnPheProGlyPheProAsnGlyIleMetGlyAlaAspLeuMetAspAsnCyArgAla 80
DB 181 AACITCCCGGATTCCTCCACCGCGCATCGGCGCGCGCGCGCGCGCGCGCGCG 240

QY 81 GlnSerLeuArgPheGlyThrAsnIleLeuSerGluThrValThrAlaValAspPheSer 100
DB 241 CAGTCGCGCTTCG 300

QY 101 AlaCysProPheArgValSerAlaAspSerThrThrValLeuAlaAspAlaValIleVal 120
DB 301 GCCCG 360

QY 121 AlaThrGlyAlaValAlaArgArgLeuHisPheProGlySerAspAlaTyTriPAsnArg 140
DB 361 GCCACG 420

QY 141 GlyIleSerAlaCysAlaValCysAspGlyAlaAlaProIlePheArgAsnLysProfile 160
DB 421 GGCAATCTCCG 480

QY 161 AlaValIleGlyGlyAlaAspSerAlaMetGluGlySerAsnPheLeuThrIleVal 180
DB 481 GCCGTCATCG 540

QY 181 SerHisValTyrIleIleHisArgArgAsnThrPheArgAlaSerLysIleMetGlnAla 200
DB 541 TCCCAAGTGTATCATCATCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 600

QY 201 ArgAlaLeuGluAsnProLysIleValLeuThrPheSerGluValValGluAlaTyr 220
DB 601 AGGCGGCTCTCCATCTTAAGATCCAGGTTGTCTCGGACTC-GAGGTGTCTCGGCGTTAC 659

QY 221 GlyGlyAlaAsnGlyGlyProLeuAlaGlyValIleValIleValIleValIleVal 240
DB 660 GCGCGTGCAGCG 719

QY 241 ValSerAspLeuGlnValSerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLys 260
DB 720 GTGTCGACTTCAGGTGTCTCGGCGCTTTCTTCGCGCATCGGCGCGCGCGCGCG 779

QY 261 PheLeuGlyGlyGlnLeuGluLeuAspSerAspGlyTyrValIleThrLysProGlySer 280
DB 780 TTTCTCAATGGCG 839

QY 281 ThrHisThrSerValIleGlyValPheAlaAlaGlyAspValGlnAspLysIleValArg 300
DB 840 ACACATACCAGTGTGA-GGGGTCTTTGTCTGTGGAGAGGTGCAGGATAAGAGTATCGT 898

QY 301 GlnAlaIleThrAlaAlaGlySerGlyCysMetAlaAlaLeu-AspAlaGluHisTyrIle 320
DB 899 CAGGCCATTACTCTCTCGATCAGGTTGATGGTGTCTTTGGGACCGCGCGCGCGCG 958

QY 320 uGlnGluIleGlyAlaGluGluGlyLysSerasp 331
DB 959 GCAGGAGGTGGGTCACAGTGGGCAAGTCTGAT 992

RESULT 2

US-09-540-014-23

Sequence 23, Application US/09540014

Patent No. 6380372

GENERAL INFORMATION:

APPLICANT: Cho, Myeong-Je

APPLICANT: Del Val, Greg

APPLICANT: Caillaud, Maxime

APPLICANT: Lemaux, Peggy G.

APPLICANT: Buchanan, Bob B.

TITLE OF INVENTION: Barley Gene for Thioresoxin and

TITLE OF INVENTION: NADP-Thioresoxin Reductase

FILE REFERENCE: 2001-0701.30

CURRENT APPLICATION NUMBER: US/09/540,014

CURRENT FILING DATE: 2000-03-31

PRIOR APPLICATION NUMBER: US 60/127,198

PRIOR FILING DATE: 1999-03-31

PRIOR APPLICATION NUMBER: US 60/169,162

PRIOR FILING DATE: 1999-12-06

PRIOR APPLICATION NUMBER: US 60/177,740

PRIOR FILING DATE: 2000-01-21

PRIOR APPLICATION NUMBER: US 60/177,739

PRIOR FILING DATE: 2000-01-21

NUMBER OF SEQ ID NOS: 51

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 23

LENGTH: 995

TYPE: DNA

ORGANISM: Hordeum vulgare

US-09-540-014-23

Alignment Scores:

Pred. No.: 7,03e-172 Length: 995

Score: 1510.00 Matches: 302

Percent Similarity: 93.98% Conservative: 10

Best Local Similarity: 90.96% Mismatches: 19

Query Match: 88.36% Indels: 3

DB: 4 Gaps: 0

US-10-005-429-25 (1-331) x US-09-540-014-23 (1-995)

QY 1 MetGluGlySerAlaAlaAlaProLeuArgThrArgIleCysIleIleGlySerGlyPro 20

DB 1 ATGGAGGATCCGCGCGCGCGCGCTCCGACAGCGGTCGATCATCGGAGCGCGCG 60

QY 21 AlaAlaHisThrAlaAlaIleTyAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 40

DB 61 GCCGCGCACACGCGCGCGCTATCCGCGCGCGCGCGAGCTCAAGCGCGCTCTTCGAG 120

QY 41 GlyTyrMetAlaAsnAspIleAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 60

DB 121 GGCTGGATGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180

QY 61 AsnPheProGlyPheProAsnGlyIleMetGlyAlaAspLeuMetAspAsnCyArgAla 80

DB 181 AACITCCCGGATTCCTCCACCGCGCATCGGCGCGCGCGCGCGCGCGCGCGCG 240

QY 81 GlnSerLeuArgPheGlyThrAsnIleLeuSerGluThrValThrAlaValAspPheSer 100

DB 241 CAGTCGCGCTTCG 300

QY 101 AlaCysProPheArgValSerAlaAspSerThrThrValLeuAlaAspAlaValIleVal 120

DB 301 GCCCG 360

QY 121 AlaThrGlyAlaValAlaArgArgLeuHisPheProGlySerAspAlaTyTriPAsnArg 140

DB 361 GCCACG 420

QY 141 GlyIleSerAlaCysAlaValCysAspGlyAlaAlaProIlePheArgAsnLysProfile 160

DB 421 GGCAATCTCCG 480

QY 161 AlaValIleGlyGlyAlaAspSerAlaMetGluGlySerAsnPheLeuThrIleVal 180

DB 481 GCCGTCATCG 540

QY 181 SerHisValTyrIleIleHisArgArgAsnThrPheArgAlaSerLysIleMetGlnAla 200

DB 541 TCCCAAGTGTATCATCATCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 600

QY 201 ArgAlaLeuGluAsnProLysIleValLeuThrPheSerGluValValGluAlaTyr 220

DB 601 AGGCGGCTCTCCATCTTAAGATCCAGGTTGTCTCGGACTC-GAGGTGTCTCGGCGTTAC 659

QY 221 GlyGlyAlaAsnGlyGlyProLeuAlaGlyValIleValIleValIleValIleVal 240

DB 660 GCGCGTGCAGCG 719

QY 241 ValSerAspLeuGlnValSerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLys 260

DB 720 GTGTCGACTTCAGGTGTCTCGGCGCTTTCTTCGCGCATCGGCGCGCGCGCGCG 779

QY 261 PheLeuGlyGlyGlnLeuGluLeuAspSerAspGlyTyrValIleThrLysProGlySer 280

DB 780 TTTCTCAATGGCG 839

QY 281 ThrHisThrSerValIleGlyValPheAlaAlaGlyAspValGlnAspLysIleValArg 300

DB 840 ACACATACCAGTGTGA-GGGGTCTTTGTCTGTGGAGAGGTGCAGGATAAGAGTATCGT 898

QY 301 GlnAlaIleThrAlaAlaGlySerGlyCysMetAlaAlaLeu-AspAlaGluHisTyrIle 320

DB 899 CAGGCCATTACTCTCTCGATCAGGTTGATGGTGTCTTTGGGACCGCGCGCGCGCG 958

QY 320 uGlnGluIleGlyAlaGluGluGlyLysSerasp 331

DB 959 GCAGGAGGTGGGTCACAGTGGGCAAGTCTGAT 992

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 5, 2004, 03:14:43 ; Search time 95.6061 Seconds
(without alignments)
1921.307 Million cell updates/sec

Title: US-10-005-429-25

Perfect score: 1709

Sequence: 1 MEGSAAPLRICIGSGP.....AALDAHYLIQIGAGKSKD 331

Scoring table: BLOSUM62

Xgapop 10.0, Xgapext 0.5

Ygapop 10.0, Ygapext 0.5

Fgapop 6.0, Fgapext 7.0

Delop 6.0, Delext 7.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO spoel_p/US10005429/runat_04052004_121650_15463/app query.fasta_1.782
-DB=Issued Patents NA -QFMT=fastap -SUPPIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blom62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10005429 @CGN_1_115 @runat_04052004_121650_15463 -NCPUS=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA.*
1: /cgn2_6/ptodata/2/ina/5A COMB.seq.*
2: /cgn2_6/ptodata/2/ina/5B COMB.seq.*
3: /cgn2_6/ptodata/2/ina/6A COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PCOTUS COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1510	88.4	995	4	US-09-540-014-10
2	1510	88.4	995	4	US-09-540-014-23
3	1478	86.5	1550	4	US-09-598-747-26
4	1290	75.5	1021	4	US-09-598-747-24
5	1217.5	71.2	998	4	US-09-540-014-26
6	929.5	54.4	1230025	4	US-09-198-452A-1
7	905	53.0	1423	1	US-08-386-729A-6
8	747	43.7	4403765	3	US-09-103-840A-2
9	747	43.7	4411529	3	US-09-103-840A-1
10	743	43.5	1443	4	US-09-321-017B-685
11	712.5	41.7	963	4	US-09-328-352-1552
12	709.5	41.5	49617	4	US-09-596-002-28

13	709	41.5	1050	4	US-09-489-039A-4925	Sequence 4925, Ap
14	705	41.3	966	4	US-09-540-014-27	Sequence 27, Appl
15	703.5	41.2	954	4	US-09-328-352-3988	Sequence 3988, Ap
16	701	41.0	972	4	US-09-252-991A-13278	Sequence 13278, A
17	701	41.0	1413	4	US-09-252-991A-12680	Sequence 12680, A
18	700.5	41.0	1020	4	US-09-543-681A-1461	Sequence 1461, Ap
19	697	40.8	1830121	4	US-09-557-884-1	Sequence 1, Appli
20	697	40.8	1830121	4	US-09-643-990A-1	Sequence 1, Appli
21	600.5	35.1	640681	4	US-09-790-988-1	Sequence 1, Appli
22	549.5	32.2	933	4	US-09-134-000C-2109	Sequence 2109, Ap
23	538.5	31.5	13086	4	US-08-956-171E-16	Sequence 16, Appl
24	507.5	29.7	2412	4	US-08-961-527-62	Sequence 62, Appl
25	480	28.1	648	4	US-09-252-991A-15129	Sequence 15129, A
26	473	27.7	987	4	US-09-134-000C-492	Sequence 492, App
27	463	27.1	666	4	US-09-252-991A-14995	Sequence 14995, A
28	437	25.6	666	4	US-09-252-991A-14492	Sequence 14492, A
29	421.5	24.7	1517	4	US-09-543-681A-318	Sequence 318, App
30	397.5	23.3	1527	4	US-09-134-001C-1733	Sequence 1733, Ap
31	394.5	23.1	762	4	US-09-134-001C-2675	Sequence 2675, Ap
32	387.5	22.7	6252	4	US-08-956-171E-50	Sequence 50, Appl
33	382.5	22.4	1809	1	US-08-220-677A-1	Sequence 1, Appli
34	372.5	21.8	1539	4	US-09-107-532A-2905	Sequence 2905, Ap
35	372	21.8	580073	4	US-08-545-528D-1	Sequence 1, Appli
36	369.5	21.6	1572	4	US-09-328-352-2268	Sequence 2268, Ap
37	369.5	21.6	1572	4	US-09-328-352-2269	Sequence 2269, Ap
38	363.5	21.3	600	4	US-09-252-991A-14870	Sequence 14870, A
39	358	20.9	1664976	4	US-08-916-421B-1	Sequence 1, Appli
40	355.5	20.8	1569	4	US-09-252-991A-11892	Sequence 11892, A
41	355.5	20.8	2526	4	US-09-252-991A-12018	Sequence 12018, A
42	351.5	20.6	751	3	US-08-998-415-219	Sequence 219, App
43	351.5	20.6	1464	4	US-09-489-039A-5743	Sequence 5743, Ap
44	321	18.8	1575	4	US-09-540-236-786	Sequence 786, Appl
45	321	18.8	19619	4	US-09-596-002-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-09-540-014-10
; Sequence 10, Application US/09540014
; Patent No. 6380372
; GENERAL INFORMATION:
; APPLICANT: Cho, Myeong-Je
; APPLICANT: Del Val, Greg
; APPLICANT: Caillaud, Maxime
; APPLICANT: Lemaux, Peggy G.
; APPLICANT: Buchanan, Bob B.
; TITLE OF INVENTION: Barley Gene for Thioredoxin and
; TITLE OF INVENTION: NADP-Thioredoxin Reductase
; FILE REFERENCE: 2001-0701.30
; CURRENT APPLICATION NUMBER: US/09/540,014
; CURRENT FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 60/127,198
; PRIOR FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: US 60/169,162
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: US 60/177,740
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 60/177,739
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 995
; TYPE: DNA
; ORGANISM: Hordeum vulgare
US-09-540-014-10
Alignment Scores:
Pred. No.: 7.03e-172 Length: 995
Score: 1510.00 Matches: 302
Percent Similarity: 93.98% Conservative: 10
Best Local Similarity: 90.98% Mismatches: 19

/clone="P0AC044"
 /tissue_type="abiotic stress treated leaf and root tissue"
 /lab_hosts="DH108-Tona"
 /clone_lib="potato abiotic stress cDNA library"
 /note="vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
 supplier: Solanum tuberosum var. Kennebec plants were
 grown from cuttings on a 16hr light/8 hr dark cycle at 25
 C for 3-4 weeks. Abiotic stress conditions were applied to
 four separate sets of plants. Set 1 involved saturation of
 the soil with 150 mM NaCl and tissues were harvested at
 following application of the salt stress (leaves: 2hr, 12hr,
 2d, 4d, and 4d; roots: 2hr, 6hr, 12hr, and 2d).
 Set 2 were grown under the standard conditions and then
 were water stressed by withdrawal of further watering
 applications. Drought stressed plants were harvested after
 cessation of watering (leaves: 3d, 5d, and 7d; roots: 3d
 and 5d). Set 3 were grown under the standard conditions
 and then were cold stressed by placement at 4 C. Cold
 stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,
 and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d,
 2d. Set 4 were grown under the standard conditions and
 then were heat stressed by placement at 35 C. Heat
 stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,
 2d and 4d and heat-stressed roots were harvested at 6 hr,
 12 hr, 1 d, and 4d. RNA was isolated from all tissues and
 equal RNA from each tissue and stress was pooled to
 construct the cDNA library. RNA sample."

ORIGIN

Alignment Scores:
 Pred. No.: 1,14e-122 Length: 981
 Score: 1206.50 Matches: 231
 Percent Similarity: 87.50% Conservative: 35
 Best Local Similarity: 75.99% Mismatches: 31
 Query Match: 70.60% Indels: 7
 DB: 14 Gaps: 2

US-10-005-429-25 (1-331) x CK270016 (1-981)

Qy 10 ArgThrArgIleCysIleGlySerGlyProAlaAlaHisThrAlaAlaIleGlyAla 29
 Db 79 AAGACCAAGTGTTCATCGAAGTGGACCGCGGCTCACACCGCGCCATTCAGCA 138
 Qy 30 AlaArgAlaGluLeuLeuProValLeuPheGluGlyTrpMetAlaAsnAspIleAla 49
 Db 139 GCAGCGCGGAGCTAAACCCATCTCTTTGAAGATGGATGGCCATGATCGGCCA 198
 Qy 50 GlyGlyGlnLeuThrThrThrAspValGluAsnPheProGlyPheProAsnGlyIle 69
 Db 199 GGTGGACAGCTCACACACCTCCGAGGTTCAGAAATTCCTCCGGTTCCCGAAGGACTC 258
 Qy 70 MetGlyAlaAspLeuMetAspAsnCysArgAlaGlnSerLeuArgPheGlyThrAsnIle 89
 Db 259 GCCGGTGTGAAGTCACTGACCGCGGTGCTCAATCTGTTTCGATTCGGTACCCAGATC 318
 Qy 90 LeuSerGluThrValThrAlaValAspPheSerAlaCysProPheArgValSerAlaAsp 109
 Db 319 TTCAGTGAACGTGAAGTAAAGTTCTCTCTGCTAGTCTCTTCCTCAAGTTCATGTCGAT 378
 Qy 110 SerThrThrValLeuAlaAspAlaValIleValAlaThrGlyAlaValAlaArgArgLeu 129
 Db 379 GAAGAGCTGTACTAGCAGAGCTGTATTATTCGCTATTCGTTGCTGTGTTCGCAAGCGGCTT 438
 Qy 130 HisPheProGlySer-----AspAlaValTrpAsnArgGlyIleSerAlaCys 145
 Db 439 GAATTCCTGGATCCGGACGGCCAAATGATATTCGATTCGCGGAGTCTCGCTGTGT 498
 Qy 146 AlaValCysAspGlyAlaAlaProIlePheArgAsnLysProIleAlaValIleGlyGly 165
 Db 499 GCTGTGTGTGACGGCGAGTCCGATCTTCGTAAACAAGCCCTTTGGCGGTGATCGGTGT 558
 Qy 166 GlyAspSerAlaMetGluGluSerAsnPheLeuThrLysTrpGlySerHisValTrpIle 185

Db 559 GCGAGTTCAGCAATCGAAGAGCTACATTTCTGACCAAAATATGTTCTCGAAAGTGTATATA 618
 Qy 186 ILeHisArgAsnThrPheArgAlaSerLysIleMetGlnAlaArgAlaLeuGluAsn 205
 Db 619 ATTCAATAGAGGATGAATTTAGGCTTCGAGATTATCGAAATAGGCATTCAGTAAC 678
 Qy 206 ProLysIleLysValLeuTrpAspSerGluValValGluAlaTrpGlyGlyAlaAsnGly 225
 Db 679 CCTAAGATAGAGTGTATTGGAATTCCTGCTGGTGGAGGCATATCGGAGAGTCT--- 735
 Qy 226 GlyProLeuAlaGlyValLysValLysAsnLeuLeuAsnGlyGluValSerAspLeuGln 245
 Db 736 -----TTGGTGGATTAAGGTGGAGATGGTTACTGGAGAGGTATCAGATTGGAG 789
 Qy 246 ValSerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLysPheLeuGlyGln 265
 Db 790 GTTTCGGTGTCTTCTTGTCTTGGCATGACCTGCTACCAATTTTGGATGGACAA 849
 Qy 266 LeuGluLeuAspSerAspGlyTrpValGluThrLysProGlySerThrHisThrSerVal 285
 Db 850 CTCAGTGTGATGCTGAGAGGTATGTTCACACCGTCCGAGGACGACAAAGACTAGCGTT 909
 Qy 286 LysGlyValPheAlaAlaGlyAspValGlnAspLysLysTrpArgGlnAlaIleThrAla 305
 Db 910 AGAGGTGTATTCTCTGCTGCTGATGTGCAAGATAGAGTACCGGCGGACGATCTGCT 969
 Qy 306 AlaGlySerGly 309
 Db 970 GCTGTTCAGGA 981

RESULT 14
 CK280506 920 bp mRNA linear EST 15-DEC-2003
 LOCUS EST743228 Nicotiana benthamiana mixed tissue cDNA library,
 DEFINITION normalized, full-length Nicotiana benthamiana cDNA clone NEMAL09 5',
 end, mRNA sequence.
 ACCESSION CK280506
 VERSION CK280506.1 GI:39850125
 KEYWORDS EST.
 SOURCE Nicotiana benthamiana
 ORGANISM Nicotiana benthamiana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; lamids; Solanales; Solanaceae; Nicotiana.
 REFERENCE 1 (bases 1 to 920)
 AUTHORS Buell, C.R., Hart, A., Zismann, V., Karanycheva, S.A., Day, B.,
 Staskawicz, B., Jin, H. and Baker, B.
 TITLE Generation of EST sequences from Nicotiana benthamiana
 JOURNAL Unpublished (2003)
 COMMENT Other ESTs: EST743227
 Contact: Robin Buell
 The Institute for Genomic Research
 9712 Medical Center Dr, Rockville, MD 20850, USA
 Email: potato-array@tigr.org
 Clones can be requested from TIGR via potato@tigr.org
 Seq primer: CAG GAA ACA GCT ATG ACC.
 Location/Qualifiers
 1..920
 /organism="Nicotiana benthamiana"
 /mol_type="mRNA"
 /db_xref="taxon:4100"
 /clone="NEMAL09"
 /tissue_type="abiotic and biotic stress-treated leaves,
 callus tissue and root tissue"
 /lab_hosts="DH108-Tona"
 /clone_lib="Nicotiana benthamiana mixed tissue cDNA
 library, normalized, full-length"
 /note="vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
 supplier: RNA was isolated from Nicotiana benthamiana
 tissues that include callus, roots from liquid culture
 grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
 cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
 challenged leaves (Pseudomonas syringae pv tomato 12 hr;

FEATURES
source

```

DEFINITION EST751943 Nicotiana benthamiana mixed tissue cDNA library,
normalized, full-length Nicotiana benthamiana cDNA clone NEMEM34 5'
end, mRNA sequence.
ACCESSION CK289221 GI:39867503
VERSION EST.
SOURCE Nicotiana benthamiana
ORGANISM Nicotiana benthamiana
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
TITLE asterids; lamids; Solanales; Solanaceae; Nicotiana.
JOURNAL 1 (bases 1 to 930)
COMMENT Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B.,
Skaskawicz, B., Jin, H. and Baker, B.
Generation of EST sequences from Nicotiana benthamiana
Unpublished (2003)
Other ESTs: EST751944
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from TIGR via potato@tigr.org
Seq primer: ATT TAG GTG ACA CTA TAG.
FEATURES
    source
        1..930
            /organism="Nicotiana benthamiana"
            /mol_type="mRNA"
            /db_xref="taxon:4100"
            /clone="NEMEM34"
            /tissue types="abiotic and biotic stress-treated leaves,
            callus tissue and root tissue"
            /lab_host="DH10B-TonA"
            /clone_lib="Nicotiana benthamiana mixed tissue cDNA
            library, normalized, full-length"
            /notes="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
            supplier: RNA was isolated from Nicotiana benthamiana
            tissues that include callus, roots from liquid culture
            grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
            cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
            challenged leaves (Pseudomonas syringae pv tomato 12 hr;
            Xanthomonas campestris pv campestris 12 hr, 18hr;
            Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
            campestris pv vesicatoria 18hr). RNA was isolated from
            these tissues and pooled in approximately equal molar
            amounts."
ORIGIN
Alignment Scores:
Pred. No.: 1,77e-124 Length: 930
Score: 1222.50 Matches: 239
Percent Similarity: 88.18% Conservative: 22
Best Local Similarity: 80.74% Mismatches: 30
Query Match: 71.53% Indels: 5
DB: 14 Gaps: 2
US-10-005-429-25 (1-331) x CK289221 (1-930)
Qy 9 LeuArgThrArgIleCysIleIleGlySerGlyProAlaAlaHisThrAlaAlaIleTyr 28
Db 51 CTAAACCCGCTCTGTATATCGGAGCGGCCCGCAGCTATACGGCCGCAATTAC 110
Qy 29 AlaAlaArgAlaGluLeuLysProValLeuPheGluGlyTrpMetAlaAsnAspIleAla 48
Db 111 GCGGCACGTCGCGAGCTGAAGCGGATTTCTTTGAAGGATGGATGGCTACGACATAGCT 170
Qy 49 AlaGlyGlyGlnLeuThrThrThrThrThrThrThrThrThrThrThrThrThrThrThr 68
Db 171 CCGGCGGCTCAGCTTTACGACACACCGGATGTGAGAACCTTTCCGGTTTCTCGAGGT 230
Qy 69 IleMetGlyAlaAspLeuMetAsnAsnCysArgAlaGlnSerLeuArgPheGlyThrAsn 88
Db 231 ATTTGGCGGTGCTGAGCTTATGGAACCGGTGCGGTGCGGAGTCCGTTCGTTTCGGGACACAA 290

```

```

Qy 89 IleLeuSerGluThrValThrAlaValAspPheSerAlaCysProPheArgValSerAla 108
Db 291 ATTCACTACTGAACCTGTAACCTAAAGGTGACCTTTCTAAAGTCCCTTTTGGAGATTGTTGG 350
Qy 109 AspSerThrThrValLeuAlaAspAlaValIleValAlaThrGlyValAlaValAlaArgArg 128
Db 351 TCTGATAGGACCTGCTAGCTGACCGCTTATTTGCTACCGGTGCTGTGCTGCTAAGCGG 410
Qy 129 LeuHisPheProGlySer-----AspAlaTyrTrpAsnArgGlyIleSerAlaCysAla 146
Db 411 CTTGACTTTTCCCGGCTCCGGCAATGACGGTTTCTGGAATAGGGGAATTTCCGCTTGTGTC 470
Qy 147 ValCysAspGlyAlaAlaProIlePheArgAlaLysProIleAlaValIleGlyGlyGly 166
Db 471 GTTTGTGACGGCGCGCTCCGATTTTAGGAATAGCCATTGCGGTGATTGTTGGTGGG 530
Qy 167 AspSerAlaMetGluGluSerAsnPheLeuThrLysTyrGlySerHisValTyrIleIle 186
Db 531 GATTGAGCTATGGAAGAGCTAATTTTGTGACTAAATATGTTCTAAAGTGTATATTATT 590
Qy 187 HisArgArgAsnThrPheArgAlaSerLysIleMetGlnAlaArgAlaLeuGluAsnPro 206
Db 591 CATAGAGGGATGAGTTTAGGGCATCGAAGATTATGCAAAAGTAGAGCATGAGTAACCT 550
Qy 207 LysIleLysValLeuTipAspSerGluValValGluAlaTyrGlyGlyAlaAsnGlyGly 226
Db 651 AAAATAGAGGTGATTTGGAACCTCAAGTGTAGTGGAGCTTATGGGAGAG----- 701
Qy 227 ProLeuAlaGlyValLysValLysAsnLeuLeuAsnGlyGluValSerAspLeuGlnVal 246
Db 702 CTATTGGGTGGATGAAGGTGAAGATGTTGTACTCGGGGAAGTTTTCGGAATTGCAAGTT 761
Qy 247 SerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLysPheLeuGlyGlyGlnLeu 266
Db 762 TCGGTTTGTGTTTTCGCAATTCGGCATGACCGCTACTAAGTTTTCGACGGGCAAGTTA 821
Qy 267 GluLeuAspSerAspGlyTyrValGluThrLysProGlySerThrHisThrSerValLys 286
Db 822 GAGTTGGATTCTGATGGGTATGTTGTGACTAAGCCGGGAGCCGACCTTGACCAAGTGTAAAG 881
Qy 287 GlyValPheAlaAlaGlyAspAlaGlnAspLysLysTyrArgGlnAla 302
Db 882 GGTGTGTTTGTGCTGCTGATGTGTCAGGATAAGAGTATAGGCAAGCT 929
RESULT 13
LOCUS CK270016
DEFINITION CK270016 981 bp mRNA linear EST 12-DEC-2003
clone FOACQ44 5' end, mRNA sequence.
ACCESSION CK270016
VERSION CK270016.1 GI:39826994
KEYWORDS EST.
SOURCE Solanum tuberosum (potato)
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum.
REFERENCE 1 (bases 1 to 981)
AUTHORS Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B.
TITLE Generation of ESTs from abiotic stressed potato tissue
JOURNAL Unpublished (2003)
COMMENT Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from TIGR via potato@tigr.org
Seq primer: ATT TAG GTG ACA CTA TAG.
FEATURES
    source
        1..981
            /organism="Solanum tuberosum"
            /mol_type="mRNA"
            /cultivar="Kennebec"
            /db_xref="taxon:4113"

```

```

Qy 186 ILeHisArgArgAsnThrPheArgAlaSerLysIleMetGlnAlaAaGAlaLeuGluAsn 205
Db 573 ATTCATAGGAGGAGTAAATTTAGGCGCTTCGAGGATTATCGGAATAGCGCATTCAGGTAC 632
Qy 206 ProLysIleLysValLeuThrAspSerGluValValGluAlaTyrGlyGlyAlaAsnGly 225
Db 633 CCTAAGATAGAGGTGATTTCGAATTCCTCTGTGTGGAGGCATATGGGGAGAACTCT--- 689
Qy 226 GlyProLeuAlaGlyValLysValLysAsnLeuLeuAsnGlyGluValSerAspLeuGln 245
Db 690 -----TTGGGTGATTAAAGGTGAGAAATGCTTACTCGAGAGGTATCAGATTGGAG 743
Qy 246 ValSerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLysPheLeuGlyGlyGln 265
Db 744 GTTTCGGGTTCCTTCTGCTATTGGGATGAACTCTGTACCAATTTTGGATGGACAA 803
Qy 266 LeuGluLeuAspSerAspGlyTyrValGluThrLysProGlySerThrHisThrSerVal 285
Db 804 CTGCAGTTGGATGCTGAGAGGTATGTTGCAACCGTCCAGGCGACGACAAAGACTAGCGTT 863
Qy 286 LysGlyValPheAlaAlaGlyAspValGlnAspLysLysTyrArgGlnAlaIleThrAla 305
Db 864 AGAGGTGATTTCCTGCTGGTGAATGTCAGATTAAGATACCGGCAAGCCATCACTGCT 923
Qy 306 AlaGlySerGlyCysMetAla 312
Db 924 GCTGTTCCAGATGATGCA 944

```

```

RESULT 11
CK252016 943 bp mRNA linear EST 12-DEC-2003
LOCUS EST735653 potato callus cDNA library, normalized and full-length
DEFINITION Solanum tuberosum cDNA clone POCBR95 5' end, mRNA sequence.
ACCESSION CK252016
VERSION CK252016.1 GI:39805600
KEYWORDS EST.
SOURCE Solanum tuberosum (potato)
ORGANISM Solanum tuberosum
REFERENCE Buell,C.R., Hart,A., Zismann,V., Karamycheva,S.A. and Baker,B.
AUTHORS 1 (bases 1 to 943)
JOURNAL Generation of ESTs from potato callus tissue
COMMENT Other ESTs: EST735654
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from TIGR via potato@tigr.org
Seq primer: Art TAG GTG ACA CTA TAG.
FEATURES
Location/Qualifiers
1..943
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="POCBR95"
/tissue_type="callus"
/lab_host="DH10B-TonA"
/clone_lib="potato callus cDNA library, normalized and full-length"
/note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI; supplier: RNA was isolated from Solanum tuberosum var. Kennebec callus tissue grown on solid media."

```

```

ORIGIN
Alignment Scores: 6.55e-126 Length: 943
Pred. No.: 1235.50 Matches: 236
Score: 88.24% Conservative: 34
Percent Similarity:

```

```

RESULT 12
CK289221
LOCUS

```

```

Best Local Similarity: 77.12% Mismatches: 29
Query Match: 72.29% Indels: 7
DB: 14 Gaps: 2
US-10-005-429-25 (1-331) x CK252016 (1-943)
Qy 10 ArgThrArgIleCysIleIleGlySerGlyProAlaAlaHisThrAlaIleThrAla 29
Db 35 AAGACAAATTTGCATCATCGGAAGTGGACCGCGGCTCACACCCGCGCATTTACGCA 94
Qy 30 AlaArgAlaGluLeuLysProValLeuPheGluGlyTyrMetAlaAsnAspIleAlaAla 49
Db 95 GCACGCGCGCGAGCTAAACCGATCCCTTTTGAAGGATGGATGCCCAATGATATCGGCCA 154
Qy 50 GlyGlyGlnLeuThrThrThrThrAspValGluAsnPheProGlyPheProAsnGlyIle 69
Db 155 GGTGGACAGCTCAACACCCCTCCGAGGTTCAGAAATTTCCCGGTTCCCGGAAGGACTC 214
Qy 70 MetGlyAlaAspLeuMetAspAsnCysArgAlaGlnSerLeuArgPheGlyThrAsnIle 89
Db 215 GCGGTGGTGAATCTCATGGACCGGTGCCGTCTCAATCTGTTCGATTCGGTACACAGATC 274
Qy 90 LeuSerGluThrThrThrAlaValAspPheSerAlaCysProPheArgValSerAlaAsp 109
Db 275 TTCACGTGAACTGTAAAGTAACGTTGATTTCTCTGTAGTCTCTTCAAAGTCATGTCGAT 334
Qy 110 SerThrThrValLeuAlaAspAlaValIleValAlaThrGlyAlaValAlaAaArgLeu 129
Db 335 GAAAGGAGCTGTACTAGCAGACGCTGTATTATTCGTACTCGTGTCTGTTCGCAAGCGGCT 394
Qy 130 HisPheProGlySer-----AspAlaTyrTyrAsnArgGlyIleSerAlaCys 145
Db 395 GAATTTCTCGATCCGCGACGCGCAAGGATTTGGATCGCGGATCTCGGCTGT 454
Qy 146 AlaValCysAspGlyAlaAlaProllePheArgAsnLysProIleAlaValIleGlyGly 165
Db 455 GCTGTGTGTGACGCGCAGCTCCGATCTTTTCGTAACAAGCCTTTGGCGGTGATCGGTGT 514
Qy 166 GlyAspSerAlaMetGluGluSerAsnPheLeuThrLysTyrGlySerHisValTyrIle 185
Db 515 GGAGATTTCAGCATTTGGAGAGCTACATTTCTACGCAATATGGTTCGAAAGTGATATA 574
Qy 186 IleHisArgArgAsnThrPheArgAlaSerLysIleMetGlnAlaArgAlaLeuGluAsn 205
Db 575 ATTCATAGGAGGATGAATTTAGGCGCTTCGAGATTATGCAATATGCGAATAGCGCATTCAGTAA 634
Qy 206 ProLysIleLysValLeuThrAspSerGluValValGluAlaTyrGlyGlyAlaAsnGly 225
Db 635 CCTAAGATAGAGGTGATTTCGAATTCCTGTGTGGAGGCATATGGGGAGAACTCT--- 691
Qy 226 GlyProLeuAlaGlyValLysValLysAsnLeuLeuAsnGlyGluValSerAspLeuGln 245
Db 692 -----TTGGGTGATTAAAGGTGAGAAATGCTTACTCGAGAGGTATCAGATTTGGAG 745
Qy 246 ValSerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLysPheLeuGlyGln 265
Db 746 GTTTCGGGTTCCTTCTGCTATTGGGATGAACCTGCTACCAATTTTGGATGGACAA 805
Qy 266 LeuGluLeuAspSerAspGlyTyrValGluThrLysProGlySerThrHisThrSerVal 285
Db 806 CTGCGTTGGATGCTCGAGAGGTATGTTGCAACCGTCCAGGCGACGACAAAGACTAGCGTT 865
Qy 286 LysGlyValPheAlaAlaGlyAspValGlnAspLysLysTyrArgGlnAlaIleThrAla 305
Db 866 AGAGGTGATTTCGCTGTGTGATGTGCAAGATAAGAAGTACCGGCAAGCCATCACTGCT 925
Qy 306 AlaGlySerGlyCysMet 311
Db 926 GCTGTTCCAGATGATG 943

```

```

930 bp mRNA linear EST 15-DEC-2003

```


QY	30	AlaArgAlaGluLeuIysProValLeuPheGluGlyTyrMetAlaAsnAspIleAlaA	49
Db	125	GCACGCGCGAGCTAAACCGATCTTTTGAAGGATGATGCCAATCATATTCGGCCCA	184
QY	50	GlyGlyGlnLeuThrThrAspValGluAsnPheProGlyPheProAsnGlyIle	69
Db	185	GGTGGACAGCTCAACACCTCCGAGGTGAGAAATTCCTCCGATTCCTCCGAGGACTC	244
QY	70	MetGlyAlaAspLeuMetAspAsnCysArgAlaGlnSerLeuArgPheGlyThrAsnIle	89
Db	245	GCCGGTGGTGAATCATGGACCGGTCGGTCAATCTGTCATTCGATTCGGTACACAGATC	304
QY	90	LeuSerGluThrValThrAlaValAspPheSerAlaCysProPheArgValSerAlaAsp	109
Db	305	TTCACTGAACCTGTAGTACCTGATTTCTCTGCCAGTCTTTCAAAGTCATGTCGGAT	364
QY	110	SerThrThrValLeuAlaAspAlaValIleValAlaThrGlyAlaValAlaArgGlu	129
Db	365	GAAGGACTGTACTAGCAGACACTGTATTATTCGTACTGCTGCTGTTCGCAAGCGCTT	424
QY	130	HisPheProGlySer-----AspAlaTyrTrpAsnArgGlyIleSerAlaCys	145
Db	425	GAATTTCTCGATCCGCGCGACCGCAATGATATTTGGATTCGCGGATCTCGGCTGC	484
QY	146	AlaValCysAspGlyAlaAlaProIlePheArgAsnLysProIleAlaValIleGlyGly	165
Db	485	GCTGTGTGTGACGGCGAGCTCCGACTTCGATACAGCTTTGGCGGTGATCGGTGT	544
QY	166	GlyAspSerAlaMetGluSerAsnPheLeuThrIysTyrGlySerHisValTyrIle	185
Db	545	GGAGATTCAGCAATGGAAGAAGCTACATCTTCTGCGAAATATGTTCCAAAGTGTATATA	604
QY	186	IleHisArgGlnThrPheArgAlaSerIleMetGlnAlaArgAlaLeuGluAsn	205
Db	605	ATTCTAGAAAGAGATTAATTTAGGCTTCGAAATATTCGAAATAGGCGATTCAGTAC	664
QY	206	ProLysIleLysValLeuTyrAspSerGluValValGluAlaTyrGlyAlaAsnGly	225
Db	665	CCTAAGATAGAGTGTATTTGGAATTTCTGCTGCTGGTGGAGCATATGGGGAGATCT--	721
QY	226	GlyProLeuAlaGlyValLysValLysAsnLeuAsnGlyGluValSerAspLeuGln	245
Db	722	-----TTGGTGGATTAAGGTTGAGATGTTGGTACTGAGAGGTTATCAGATTTGGAG	775
QY	246	ValSerGlyLeuPheAlaIleGlyHisGluProAlaThrLysPheLeuGlyGlyGln	265
Db	776	GTTTCGGGTTTGTCTTGTATTTGGCATGAACCTGTACCAATTTTGGATGACAA	835
QY	266	LeuGluLeuAspSerAspGlyTyrValGluThrLysProGlySerThrHisThrSerVal	285
Db	836	CTGCAGTTGGATGCTGAGAGGTATGTTGCAACCGTGCAGGACGACAAAGACTAGCGTA	895
QY	286	LysGlyValPheAlaAlaGlyAspValGlnAspLysLysTyrArgGlnAlaIleThrAla	305
Db	896	AGAGGTGATTTGCTGCTGATGTCAGATGAAGATGACCGGACGACATCATCTGCT	955
QY	306	AlaGlySerGlyCysMetAlaAlaLeuAspAlaGlu	317
Db	956	GCTGGTTCAGATGCATGGCAGCGTTGGATGCAGAG	991
RESULT 10			
CK258706			
LOCUS			
DEFINITION			
EST742343 potato callus cDNA library, normalized and full-length			
Solanum tuberosum cDNA clone POCDF49 5' end, mRNA sequence.			
ACCESSION			
CK258706			
VERSION			
CK258706.1 GI:39815686			
KEYWORDS			
EST.			
SOURCE			
Solanum tuberosum (potato)			
ORGANISM			
Solanum tuberosum			
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;			

asterids; lamids; Solanales; Solanaceae; Solanum.			
1 (bases 1 to 946)			
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B.			
Generation of ESTs from potato callus tissue			
Unpublished (2003)			
Other ESTs: EST742344			
Contact: Robin Buell			
The Institute for Genomic Research			
9712 Medical Center Dr, Rockville, MD 20850, USA			
Email: potato-array@tigr.org			
Clones can be requested from TIGR via potato@tigr.org			
Seq primer: ATT TAG GTG ACA CTA TAG.			
Location/Qualifiers			
1..946			
/organism="Solanum tuberosum"			
/mol_type="mRNA"			
/cultivar="Kennebec"			
/db_xref="taxon:4113"			
/clone="POCDF49"			
/tissue_type="callus"			
/lab_host="DH10B-TonA"			
/clone_lib="potato callus cDNA library, normalized and			
full_length"			
/note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;			
supplier: RNA was isolated from Solanum tuberosum var.			
Kennebec callus tissue grown on solid media."			
ORIGIN			
Alignment Scores:			
Pred. No.: 2,378-126 Length: 946			
Score: 1239.50 Matches: 237			
Percent Similarity: 88.27% Conservative: 34			
Best Local Similarity: 77.20% Mismatches: 29			
Query Match: 72.53% Indels: 7			
DB: 14 Gaps: 2			
US-10-005-429-25 (1-331) x CK258706 (1-946)			
QY	10	ArgThrArgIleCysIleIleGlySerGlyProAlaAlaHisThrAlaIleTyrAla	29
Db	33	AAAGCAAAAGTTTGCATCATCGAAGTGGACGGCGCTCACACCGCCGCCATTTACGCA	92
QY	30	AlaArgAlaGluLeuLysProValLeuPheGluGlyTyrMetAlaAsnAspIleAlaA	49
Db	93	GCACGCGCGAGCTAAACCGATCTTTTGAAGGATGGATGCCAATGATATCGCGCCA	152
QY	50	GlyGlyGlnLeuThrThrThrAspValGluAsnPheProGlyPheProAsnGlyIle	69
Db	153	GGTGGACAGCTCACACCACTCCGAGGTGAGAAATTTCCCGGTTTCCCGAAGACTC	212
QY	70	MetGlyAlaAspLeuMetAspAsnCysArgAlaGlnSerLeuArgPheGlyThrAsnIle	89
Db	213	GCGGGTGGTGAATCATGAGCGGTGCGTGTCTCATCTGTTGATTCGGTACACAGATC	272
QY	90	LeuSerGluThrValThrAlaValAspPheSerAlaCysProPheArgValSerAlaAsp	109
Db	273	TTCACTGAACCTGTAAAGTAACTGTTGATTTCTCTGCTAGTCTTTCAAAGTCATGTCGAT	332
QY	110	SerThrThrValLeuAlaAspAlaValIleValAlaThrGlyAlaValAlaArgArgLeu	129
Db	333	GAAGGACTGTACTAGCAGACGCTGTTATTATTCGCTACTGCTGCTGCTGCTGCTGCT	392
QY	130	HisPheProGlySer-----AspAlaTyrTrpAsnArgGlyIleSerAlaCys	145
Db	393	GAATTTCTCGATCCGCGCGCGCAATGATATTTGGATTCGCGGATCTCGGCTGT	452
QY	146	AlaValCysAspGlyAlaAlaProIlePheArgAsnLysProIleAlaValIleGlyGly	165
Db	453	GCTGTGTGTGACGGCGCAGCTCCGATCTTTTCGTAACAGACCTTTGGCGGTGATCGGTGT	512
QY	166	GlyAspSerAlaMetGluSerAsnPheLeuThrLysTyrGlySerHisValTyrIle	185
Db	513	GGAGATTCAGCAATGGAAGAAGCTACATTTCTGACGAAATATGTTTCGAAAGTGTATATA	572

Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@igr.org
Clones can be requested from TIGR via potato@tigr.org
Seq primer: ATT TAG GTG ACA CTA TAG.

FEATURES

Location/Qualifiers
1..970
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="POB690"
/tissue_type="abiotic stress treated leaf and root tissue"
/lab_host="PH10B-Tona"
/clone_lib="potato abiotic stress cDNA library"
/supplier: "Solanum tuberosum var. Kennebec plants were grown from cuttings on a 16hr light/8 hr dark cycle at 25 C for 3-4 weeks. Abiotic stress conditions were applied to four separate sets of plants. Set 1 involved saturation of the soil with 150 mM NaCl and tissues were harvested at following application of the salt stress (leaves: 2hr, 6hr, 12hr, 1d, 2d, and 4d; roots: 2hr, 6hr, 12hr, and 2d). Set 2 were grown under the standard conditions and then were water stressed by withdrawal of further watering applications. Drought stressed plants were harvested after cessation of watering (leaves: 3d, 5d, and 7d; roots: 3d and 5d). Set 3 were grown under the standard conditions and then were cold stressed by placement at 4 C. Cold stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d, and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d, 2d. Set 4 were grown under the standard conditions and then were heat stressed by placement at 35 C. Heat stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d, 2d and 4d and heat-stressed roots were harvested at 6 hr, 12 hr, 1 d, and 4d. RNA was isolated from all tissues and equal RNA from each tissue and stress was pooled to construct the cDNA library. RNA sample."

ORIGIN

Alignment Scores:
Pred. No.: 6 99e-129 Length: 970
Score: 1262.50 Matches: 249
Percent Similarity: 88.10% Conservative: 25
Best Local Similarity: 80.06% Mismatches: 31
Query Match: 73.87% Indels: 6
DB: 14 Gaps: 2

US-10-005-429-25 (1-331) x CK278585 (1-970)

QY 9 LeuArgThrArgIleCysIlelleGlySerGlyProAlaAlaHisThrAlaAlaIleTyr 28
DB 49 CTAATAAAGTAGCGTTTGTATATCGGAGTGGCGCTGCAGCTCACACAGTGCATTAC 108
QY 29 AlaAlaArgAlaGluLeuLysProValLeuPheGluGlyTrpMetAlaAsnAspIleAla 48
DB 109 GCAGCCGCGGAGCTTGAAGCGATCTTTTCAGAGAGTGGATGATGATGATGATGATGAT 168
QY 49 AlaGlyGlyGlnLeuThrThrThrThrThrThrThrThrThrThrThrThrThrThrThr 69
DB 169 CCGCGGGTCCAGCTTACGAC 228
QY 69 IleMetGlyAlaAspLeuMetAspAsnCysArgAlaGlnSerLeuArgPheGlyThrAsn 88
DB 229 ATTGGCGCGGAGCTTATGAAAAGTGTGGGCGAGTCTGTCTTTTGGGACACAA 288
QY 89 IleLeuSerGluThrValThrAlaValAspPheSerAlaCysProPheArgValSerAla 108
DB 289 ATTATCTACTGAACCGTACTAAGTTGATTTTCTAAAGTCTTTTAAAGTTGTTCT 348
QY 109 AspSerThrThrValLeuAlaAspAlaValIleValAlaThrGlyAlaValAlaArgArg 128

DB 349 GATGATAGGACTGATATTAGCTGACGCCGCTTATTCTCGCTACTGGTCTGTGGCTTAAGAGG 408
QY 129 LeuHisPheProGlySer-----AspAlaTyrTTPAsuAlaGlyIleSerAlaCysAla 146
DB 409 CTTGAATTCGCCGCTCCGCAATAATCGCTTCTCGAATAAGGGATATCAGCTTGGCC 468
QY 147 ValCysAspGlyAlaAlaProIlePheArgAsnLysProIleAlaValIleGlyGly 166
DB 469 GTTCTGATGGTGTGCTGCCCGATATTCGTAATAAGCAATAGCTGTAAATGGTGTGA 528
QY 167 AspSerAlaMetGluGlnSerAsnPheLeuThrLysTyrGlySerHisValTyrIleIle 186
DB 529 GATTCTGCTATGGAAGAAGCTAAATTTTAACTAATAATGTTCCGAAAGTGTATATTATT 588
QY 187 HisArgArgAsnThrPheArgAlaSerLysIleMetGlnAlaArgAlaLeuGluAsnPro 206
DB 589 CATAGGAGGATGAATTTAGGGCATCGAAGATAATGCAAAATAGGCCATTGAGTAACCT 648
QY 207 LysIleLysValLeuThrAspSerGluValValGluAlaTyrGlyAlaAsnGlyGly 226
DB 649 AAAATAGAGGTGATTGGAAATTTCTACTAGTGGAGGCTTATGGGGAAG----- 699
QY 227 ProLeuAlaGlyValLysValLysAsnLeuLeuAsnGlyGluValSerAspLeuGlnVal 246
DB 700 CTTTGGGTGGATTGCAAGTGAAATAATCTTACAGGAGAGTTTCTGATTGAATGTT 759
QY 247 SerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLysPheLeuGlyGlyGlnLeu 266
DB 760 TCAGGCTTGTGTTTTCGCCAATTCGCAACCAACAGTCAACCAATTTTGGTAAGCAATTA 819
QY 267 GluLeuAspSerAspGlyTyrValGluThrLysProGlySerThrHisThrSerValLys 286
DB 820 GAGTTGGATTTCGATGGATTTGTTTAACTAAGCGGGGACGACACTGACCACTGTAGG 879
QY 287 -GlyValPheAlaAlaGlyAspValGlnAspLysTyrArgGlnAlaIleThrAlaAla 306
DB 880 GGCTGTTTGTGCTGCTGGTGATGTCAGGATAAGAAGTAGGCAAGCTATTACTGCTGC 939
QY 306 aclySerGlyCysMetAlaAlaLeuAspAla 316
DB 940 TGGCTCAGGGTGCATGGCGGCTTTGGATGCT 970

RESULT 8
CK286466 947 bp mRNA linear EST 15-DEC-2003
LOCUS EST749188 Nicotiana benthamiana mixed tissue cDNA library.
DEFINITION normalized, full-length Nicotiana benthamiana cDNA clone NBMB229 5' end, mRNA sequence.
ACCESSION CK286466
VERSION CK286466.1 GI:39862056
KEYWORDS EST.
SOURCE Nicotiana benthamiana
ORGANISM Nicotiana benthamiana
REFERENCE 1 (bases 1 to 947)
AUTHORS Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B., Staskiewicz, B., Jin, H. and Baker, B.
TITLE Generation of EST sequences from Nicotiana benthamiana
JOURNAL Unpublished (2003)
COMMENT Other ESTs: EST749189
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@igr.org
Clones can be requested from TIGR via potato@tigr.org
Seq primer: ATT TAG GTG ACA CTA TAG.
FEATURES
source 1..947
/organism="Nicotiana benthamiana"
/mol_type="mRNA"
/db_xref="taxon:4100"

```

Qy 307 GlySerGlyCysMetAlaAlaLeuAspAlaGluHis 318
Db 944 GGCTCAGGGTGCATGGCAGCTTATAGATCCCGAAT 979

RESULT 6
CK289722
LOCUS EST752444 Nicotiana benthamiana mixed tissue cDNA library,
DEFINITION normalized, full-length Nicotiana benthamiana cDNA clone NEMB82 5',
end, mRNA sequence.
ACCESSION CK289722
VERSION CK289722.1 GI:39868489
KEYWORDS EST.
SOURCE Nicotiana benthamiana
ORGANISM Nicotiana benthamiana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiales; Solanales; Solanaceae; Nicotiana.
1 (bases 1 to 976)
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B.,
Staskiewicz, B., Jin, H. and Baker, B.
Generation of EST sequences from Nicotiana benthamiana
Unpublished (2003)
Other ESTs: EST752445
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from TIGR via potato@tigr.org
Seq primer: ATT TAG GTG ACA CTA TAG.
Location/Qualifiers
1..976
/organism="Nicotiana benthamiana"
/mol_type="mRNA"
/db_xref="taxon:4100"
/clone="NEMB82"
/tissue_type="abiotic and biotic stress-treated leaves,
callus tissue and root tissue"
/lab_host="DH10B-Tona"
/clone_lib="Nicotiana benthamiana mixed tissue cDNA
library, normalized, full-length"
/notes="RNA was isolated from Nicotiana benthamiana
tissues that include callus, roots from liquid culture
grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
challenged leaves (Pseudomonas syringae pv tomato 12 hr;
Xanthomonas campestris pv campestris 12 hr, 18hr;
Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
campestris pv vesicatoria 18hr). RNA was isolated from
these tissues and pooled in approximately equal molar
amounts."

ORIGIN
Alignment Scores:
Pred. No.: 1.97e-129 Length: 976
Score: 1267.50 Matches: 249
Percent Similarity: 88.39% Conservative: 25
Best Local Similarity: 80.3% Mismatches: 30
Query Match: 74.1% Indels: 6
DB: 14 Gaps: 2

US-10-005-429-25 (1-331) x CK289722 (1-976)

Qy 9 leuArgThrArgIleCysIleIleGlySerGlyProAlaAlaHisThrAlaAlaIleTyr 28
Db 56 CTTAAACCCGCTCTGATATATCGGACGCGCGCGAGCTCATACAGCCGCTTAC 115
Qy 29 AlaAlaArgAlaGluLeuLysProValLeuPheGluGlyTyrMetAlaAsnAspIleAla 48
Db 116 GCGGACGTCGCCAGCTAAAGCGGATCTCTTTGAAGGATGATGGCTAACGACATAGT 175
Qy 49 AlaGlyGlyClnLeuThrThrThrThrThrThrThrThrThrThrThrThrThrThrThr 68

176 CCGGGTGGTCAAGTTACGACACCCAGCGTCGAGACATTTCCCGGTTTCCCTGAGGT 235
69 IleMetGlyAlaAspLeuMetAspCysArgAlaGlnSerLeuArgPheGlyThrAsn 88
236 ATTGGCGGTGGTGAAGTATGGAACGGTCCGTCGACGCTGTGTTTCCGGACTCAA 295
89 IleLeuSerGluThrValThrAlaValAspPheSerAlaCysProPheArgValSerAla 108
296 ATTCACTACTAACTGTAATGAACTGACTTTTCTAAAAGTCCCTTTTGAGATTGTTGG 355
109 AspSerThrThrValLeuAlaAspAlaValIleValAlaThrGlyAlaValAlaArg 128
356 TCTGATAGGACTGTGTAGCTGAGCGCTCAATGTTGCTACCGTCTGTAGCTAAGCG 415
129 LeuHisPheProGlySer-----AspAlaTyrTTPAsnArgGlyIleSerAlaCysAla 146
416 CTTGAATTTCCCGGCTCCGCAATGACGGGTCTTGGATAGGGGAAATTTCCGGTTGTGCC 475
147 ValCysAspGlyAlaAlaProIlePheArgAsnLysProIleAlaValIleGlyGly 166
476 GTTGTGACGTCGCGCTCCGATTTTGGATATAGCCGTTGCGGCTGATTTGGTGGTGG 535
167 AspSerAlaMetGluGluSerAsnPheLeuThrLysTyrGlySerHisValTyrIle 186
536 GATTGACCAATGGAAGAAGCTAATTTTGGACTAAATATCGTTCTAAAGTGTATATT 595
187 HisArgAsnThrPheArgAlaSerLysIleMetGlnAlaArgAlaLeuGluAsnPro 206
596 CATAGGAGGATGAGTTAGGGCATTCAGATTTATGCAAGTAGAGATGATGATGATTA 655
207 LysIleLysValLeuTrpAspSerGluValValGluAlaTyrGlyGlyAlaAsnGly 226
656 AATATAGAGTGATTGGAACTCAAGTGTAGTGGAGCTTATGGGAGAAG----- 706
227 ProLeuAlaGlyValLysValLysAsnLeuAsnGlyGluValSerAspLeuGlnVal 246
707 CTATTGGTGGATGGAAGTGAAGATTTGTTTCTAGTGGGCAAGTTTCGATTTCAGGTT 766
247 SerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLysPheLeuGlyGlyGln 266
767 TCGGTTTGTGTTTTCGCAATGGCATGAACCACTACTAAGTTTTCGATGGGAGCTTA 826
267 GluLeuAspSerAspGlyTyrValGluThrLysProGlySerThrHisThrSerVal 286
827 GAATTCGATTCGATGGGTATGTGTGCACTAATCCCGGAACGACGTTGACGAGTTTAG 886
286 sGlyValPheAlaAlaGlyAspValGlnAspLysLysTyrArgGlnAlaIleThrAla 306
887 GGGGTGTTTGTCTCTCTGATGTGCGAGTAAAGATACAGGACAGCTATTACAGCTGC 946
306 aGlySerGlyCysMetAlaAlaLeuAsp 315
947 TGGTTCAAGGTGCGATGGCAGCTTAGAT 974

RESULT 7
CK278585
LOCUS EST724663 potato abiotic stress cDNA library Solanum tuberosum cDNA
DEFINITION clone POAE690 5' end, mRNA sequence.
ACCESSION CK278585
VERSION CK278585.1 GI:39835563
KEYWORDS EST.
SOURCE Solanum tuberosum (potato)
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiales; Solanales; Solanaceae; Solanum.
1 (bases 1 to 970)
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B.
Generation of ESTs from abiotic stressed potato tissue
Unpublished (2003)
Other ESTs: EST724664

```

```

Db      543 AGGAGGGATGAGTTTGGGCGATCCAGAGATTATGCAAAAGTAGAGCATTTGAGTAACCCCTAAA 602
Qy      208 IleValLeuThrPaspSerGluValGluAlaTyrGlyGlyAlaAsnGlyGlyPro 227
Db      603 ATAGAGTGGATTGGAACTCAAGTGTAGTGGAGCTTATGGGAGAG-----CTA 653
Qy      228 LeuAlaGlyVallysVallysAsnLeuLeuAsnGlyGluValSerAspLeuGlnValSer 247
Db      654 TTGGTGGGATTGAAGTGAAGATTTGTTACTGGGCAAGTTTCGGATTTCGAGGTTTCG 713
Qy      248 GlyLeuPhePheAlaIleGlyHisGluProAlaThrIrysPheLeuGlyGlyGlnLeuGlu 267
Db      714 GGTGTGTTTTCCCATGTCGCAATGACCGAGCTACTAGTGTGATGGGCGAGTAGAA 773
Qy      268 LeuAspSerAspGlyTyrValGluThrLysProGlySerThrHisThrSerVallysGly 287
Db      774 TTGGATTCTGATGCTATGTTGTGACTAATCCGGGAACGAGCTTGACCAAGTGTAGGGGT 833
Qy      288 ValPheAlaAlaGlyAspValGlnAspLysLysTyrArgGlnAlaIleThrAlaAlaGly 307
Db      834 GTGTTTGTCTGCTGATGTGCGAGGATAAGAGTACAGGCAAGCTATTACAGCTGCTGCT 893
Qy      308 SerGlyCysMetAlaAlaLeuAspAlaGluHisTyrLeuGlnIleGly 324
Db      894 TCAGGGTGATGTCAGCTTTAGATGCGACATTAATTCGCAAGAAATTGCT 944

RESULT 5
LOCUS   CK283459
DEFINITION Nicotiana benthamiana mixed tissue cDNA library.
          EST746181 Nicotiana benthamiana cDNA clone NEMAH16 5'
          end, mRNA sequence.
ACCESSION CK283459
VERSION   CK283459.1 GI:39856092
KEYWORDS EST.
SOURCE   Nicotiana benthamiana
ORGANISM Nicotiana benthamiana
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots;
          asterids; lamids; Solanales; Solanaceae; Nicotiana.
REFERENCE 1 (bases 1 to 981)
          Staskiewicz,B., Jin,H. and Baker,B.
          Generation of EST sequences from Nicotiana benthamiana
          Unpublished (2003)
          Other ESTs: EST746182
          Contact: Robin Buell
          The Institute for Genomic Research
          9712 Medical Center Dr, Rockville, MD 20850, USA
          Email: potato-array@tigr.org
          Clones can be requested from TIGR via potato@tigr.org
          Seq primer: ATT TAG GTG ACA CTA TAG.
FEATURES             Location/Qualifiers
     source            1..981
                     /organism="Nicotiana benthamiana"
                     /mol_type="mRNA"
                     /db_xref="taxon:4100"
                     /clone="NEMAH16"
                     /tissue_type="abiotic and biotic stress-treated leaves,
                     callus tissue and root tissue"
                     /lab_host="DH10B-TonA"
                     /clone_lib="Nicotiana benthamiana mixed tissue cDNA
                     library, normalized, full-length"
                     /notes="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
                     supplier: RNA was isolated from Nicotiana benthamiana
                     tissues that include callus, roots from liquid culture
                     grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
                     cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
                     challenged leaves (Pseudomonas syringae pv tomato 12 hr;
                     Xanthomonas campestris pv campestris 12 hr, 18hr;
                     Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
                     campestris pv vesicatoria 18hr). RNA was isolated from
                     these tissues and pooled in approximately equal molar

```

```

amounts."
ORIGIN
Alignment Scores:
Pred. No.:      1,58e-133      Length:      981
Score:          1304.50      Matches:    255
Percent Similarity: 88.78%      Conservatives: 22
Best Local Similarity: 81.73%      Mismatches: 30
Query Match:    76.33%      Indels:    5
DB:             14      Gaps:      2

US-10-005-429-25 (1-331) x CK283459 (1-981)
Qy      9 LeuArgThrArgIleCysIleIleGlySerGlyProAlaAlaHisThrAlaAlaIleTyr 28
Db      53 CTAATAAACCGGCTCTGTATCATCGGCAGCGCCCGCAGCTCATACGCCGCCCAATTTAC 112
Qy      29 AlaAlaArgAlaGluLeuLysProValLeuPheGluGlyTyrMetAlaAsnAspIleAla 48
Db      113 GCGGCACGTGCGCAGCTGAAGCCGATTCTCTTTGAGGATGAGTGGCTAACGCATAGCT 172
Qy      49 AlaGlyGlyGlnLeuThrThrThrAspValGluAsnPheProGlyPheProAsnGly 68
Db      173 CCGCGCGGTACGCTTACGACCAACCGATGTCGAGAACCTTCCCGGTTTCTCGAAGGT 232
Qy      69 IleMetGlyAlaAspLeuMetAspAsnCysArgAlaGlnSerLeuArgPheGlyThrAsn 88
Db      233 ATTGGCGGTGGTGGAGCTGATGAACGGTCCCGTGGCAGTCCGTTCGTTTCGGGACACA 292
Qy      89 IleLeuSerGlyThrValThrAlaValAspPheSerAlaCysPropheArgValSerAla 108
Db      293 ATTATACATACTGAACCTGTAACCTAAAGTGACTTTCTAAAAGTCCCTTTTCAGATTGTT 352
Qy      109 AspSerThrThrValLeuAlaAspAlaValIleValAlaThrGlyAlaValAlaArgGly 128
Db      353 TCTGATAGAGCTGTCTAGCTGACCGCGTTATTTGTGTACCGGTCTGTGCTGAAGCGG 412
Qy      129 LeuHisPheProGlySer-----AspAlaTyrTyrAsnArgGlyIleSerAlaCysAla 146
Db      413 CTTGACTTTCCCGGCTCCGGCAATGACGGGTCTCGAATAGGGAATTTTCGGCTTGTGCC 472
Qy      147 ValCysAspGlyAlaAlaProllePheArgAsnLysProIleAlaValIleGlyGly 166
Db      473 GTTGTGACGGCGCGCTCCGATTTTATAGGAATAAGCCATTGCGCGTGAATGTTGTTGG 532
Qy      167 AspSerAlaMetGluGluSerAsnPheLeuThrLysTyrGlySerHisValTyrIleIle 186
Db      533 GATTACGCTATGCAAGAGCTAATTTTGTGACTAATATGTTCTAAAGTGTATATTAT 592
Qy      187 HisArgArgAsnThrPheArgAlaSerLysIleMetGlnAlaAlaArgAlaLeuGluAsnPro 206
Db      593 CATAGAGGGATGAGTTTAGGGCATCGAAGATTATGCAAAAGTAGAGCAATTGAGTAACCC 652
Qy      207 LysIleLysValLeuThrPaspSerGluValGluAlaTyrGlyGlyAlaAsnGlyGly 226
Db      653 AAAATAGAGGTGATTGTGAACCTCAAGTGTAGTGGAGGCTTATGGGAGAG----- 703
Qy      227 ProLeuAlaGlyVallysVallysAsnLeuLeuAsnGlyGluValSerAspLeuGlnVal 246
Db      704 CTAATTGGGTGATTGAGGTGAGGTGAGATGTTGTTACTGGGGAAGTTTCGGATTTCAGGTT 763
Qy      247 SerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLysPheLeuGlyGlyGlnLeu 266
Db      764 TCGGGTTTGTGTTTTCGCCATTCGGCATGAACCCGCTACTAAGTTTTTTGACCGGCGAGTTA 823
Qy      267 GluLeuAspSerAspGlyTyrValGluThrLysProGlySerThrHisThrSerVallys 286
Db      824 GAGTTGGATTCTGATGGGTATGTTGTGACTAAGCCGGGAGCACCTTGTGCCAGTGTATAG 883
Qy      287 GlyValPheAlaAlaGlyAspValGlnAspLysLysTyrArgGlnAlaIleThrAlaAla 306
Db      884 GGTGTGTTTGTCTGCTGATGTCAGGATAGAGATATAGGCAAGCTATTACAGCTGCT 943

```

QY 89 IleLeuSerGluThrValThrAlaValAspPheSerAlaCysProPheArgValSerAla 108
Db 288 ATTCATACCTGAACCTGTAACCTGACCTTTCTAAAGTCTTTTGAGATTGTTTCG 347
QY 109 AspSerThrValLeuAlaAspAlaValIleValAlaThrGluValAlaArgArg 128
Db 348 TCTGATAGACTGTGCTAGCTGACCGCTTATTGTTGCTACGGTGTGCTGCTGCTG 407
QY 129 LeuHisPheProGlySer-----AspAlaTyrrTrpAsnArgGlyIleSerAlaCysAla 146
Db 408 CTTGACTTTCCCGGCTCGCGCAATGACGGTTCCTGGAATAGGGAAATTCGGCTGTGTC 467
QY 147 ValCysAspGluAlaAlaProIlePheArgAsnLysProIleAlaValIleGlyGlyGly 166
Db 468 GTTGTGACGGCGCGCTCCGATTTHAGCAATAGCCATTCGCGGTGATTCGTGGTGGG 527
QY 167 AspSerAlaMetGluGluSerAsnPheLeuThrLysTyrrGlySerHisValTyrrIle 186
Db 528 GATTTCAGCTATGCAAGAACTAAATTTTCTGCTAAATATGCTTCTAAAGTGTATATT 587
QY 187 HisArgArgAsnThrPheArgAlaSerLysIleMetGlnAlaArgAlaLeuGluAsnPro 206
Db 588 CATAGAGGGATGAGTTTAGGCGCATCGAAGATTATGCAAGTAGAGCAATTGATTAACCT 647
QY 207 LysIleLysValLeuTrpAspSerGluValValGluAlaTyrrGlyGlyAlaAsnGlyGly 226
Db 648 AAAATAGAGTGATTTGGCACTCAAGTGTAGTGGAGGCTTATGGGGAGAG----- 698
QY 227 ProLeuAlaGlyValLysValLysAsnLeuLeuAsnGlyGluValSerAspLeuGlnVal 246
Db 699 CTAATTGGGTGGATGCAAGGTGAAGATGTTTACTGGGGAAGTTTCGATTTGCGAGTT 758
QY 247 SerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLysPheLeuGlyGlyGlnLeu 266
Db 759 TCGGGTTGTTTTCGCCATGCGCATGCAAGTGTAGTGGAGGCTTATGGGGAGAGTTA 818
QY 267 GluLeuAspSerAspGlyTyrrValGluThrLysProGlySerThrHisThrSerValLys 286
Db 819 GAGTTGGATTCTGATGGGTATGTTGCTAAGCCGGGAGCACCCTTGACCAGTGTAAAG 878
QY 287 GlyValPheAlaAlaGlyAspValGlnAspLysLysTyrrArgGlnAlaIleThrAlaAla 306
Db 879 GGTGTGTTGCTGCTGGTGTGATGTGAGATAGAGATAGTATAGCAAGCTATTACAGTCT 938
QY 307 GlySerGlyCysMetAlaAlaLeuAspAlaGluHisTyrrLeuGlnGlu 322
Db 939 GGCTCAGGTGTGATGGCAGCTTAGATGCCGAACATTACTTCAAGAA 986

RESULT 4
CK292570
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

CK292570 946 bp mRNA linear EST 15-DEC-2003
EST755284 Nicotiana benthamiana mixed tissue cDNA library,
normalized, full-length Nicotiana benthamiana cDNA clone NEMCA40 5',
end, mRNA sequence.
CK292570.1 GI:39874140
CK292570
EST.
Nicotiana benthamiana
Nicotiana benthamiana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Nicotiana.
1 (bases 1 to 946)
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B.,
Staskawicz, B., Jin, H., and Baker, B.
Generation of EST sequences from Nicotiana benthamiana
Unpublished (2003)
Other ESTs: EST755285
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@igr.org
Clones can be requested from TIGR via potato@igr.org

Seq primer: ATT TAG GTG ACA CTA TAG.
Location/Qualifiers
1. 946
/organism="Nicotiana benthamiana"
/mol_type="mRNA"
/db_xref="taxon:4100"
/clone="NEMCA40"
/tissue_type="abiotic and biotic stress-treated leaves,
callus tissue and root tissue"
/lab_host="DH10B-Tona"
/clone_lib="Nicotiana benthamiana mixed tissue cDNA
library, normalized, full-length"
/note="vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
supplier: RNA was isolated from Nicotiana benthamiana
tissues that include callus, roots from liquid culture
grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
challenged leaves (Pseudomonas syringae pv tomato 12 hr;
Xanthomonas campestris pv campestris 12 hr, 18hr;
Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
campestris pv vesicatoria 18hr). RNA was isolated from
these tissues and pooled in approximately equal molar
amounts."

ORIGIN
Alignment Scores:
Pred. No.: 9,11e-136 Length: 946
Score: 1324.50 Matches: 257
Percent Similarity: 88.96% Conservative: 25
Best Local Similarity: 81.07% Mismatches: 30
Query Match: 77.50% Indels: 5
Gaps: 2
DB: 14
US-10-005-429-25 (1-331) x CK292570 (1-946)
QY 10 ArgThrArgIleCysIleIleGlySerGlyProAlaAlaHisThrAlaAlaIleTyrrAla 29
Db 3 AAAACCCGCCCTCTGTATCATCGGAGCGGCCCGCAGCTCATACAGCGCCATTACGCC 62
QY 30 AlaArgAlaGluLeuLysProValLeuPheGluGlyTrpMetAlaAsnAspIleAlaAla 49
Db 63 GCACGTCGCGAGCTAAAGCCGATTCCTCTTTGAAGATGGATGGCTAAACGATAGCTCCC 122
QY 50 GlyGlyGlnLeuThrThrThrAspValGluAsnPheProGlyPheProAsnGlyIle 69
Db 123 GGTGGTCAGCTTACGACCAACCCAGCTCGAGAACCTTCCCGGTTTCCCTGGAAGTATT 182
QY 70 MetGlyAlaAspLeuMetAspAsnCysArgAlaGlnSerLeuArgPheGlyThrAsnIle 89
Db 183 GGCGGTGGTGAGCTTATGGAACGGTGCCTGGCGAGTCTGTTCTGCGGACCTCAAAAT 242
QY 90 LeuSerGluThrValThrAlaValAspPheSerAlaCysProPheA-gValSerAlaAsp 109
Db 243 CATACTGAACCTGTAACCTGAAAGTTGATCTTTCTAAAAGTCTCTTTTGAGATTGTTTCGCT 302
QY 110 SerThrThrValLeuAlaAspAlaValIleValAlaThrGlyAlaValAlaArgGlu 129
Db 303 GATAGGACTGTGTAGCTGAAGCCGCTCATTTGTTCTACCGCTGCTGTAGCTTAAGCGGCT 362
QY 130 HisPheProGlySer-----AspAlaTyrrTrpAsnArgGlyIleSerAlaCysAlaVal 147
Db 363 GAATTTCCCGGCTCCCGCAATGACGGTTCCTGGAATAGGGAAATTCGGCTGTGCGGCT 422
QY 148 CysAspGlyAlaAlaProIlePheArgAsnLysProIleAlaValIleGlyGlyAsp 167
Db 423 TGTACGGTGGCGCTCGATTTTATAGGAATAGCCGCTGGCGGTGATTTGGTGGGGAT 482
QY 168 SerAlaMetGluGluSerAsnPheLeuThrLysTyrrGlySerHisValTyrrIleHis 187
Db 483 TCAGCAATGGAAGAGCTAAATTTTGTGCTAAATATGCTTCTAAAGTGTATATTATCAT 542
QY 188 ArgArgAsnThrPheArgAlaSerLysIleMetGlnAlaArgAlaLeuGluAsnProLys 207

/clone lib="ZM_0.7.1.5 kb"
/note="Vector: pBSK-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

ORIGIN

Alignment Scores:

Pred. No.: 1,62e-145 Length: 871
Score: 1412.00 Matches: 273
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 82.62% Indels: 0
DB: 29 Gaps: 0

US-10-005-429-25 (1-331) x CG300268 (1-871)

```
QY 1 MetGluGlySerAlaAlaAlaProLeuArgThrArgIleCysIleIleGlySerGlyPro 20
DB 52 ATGGAGGATCCGCGCGCTCCGCTCCGCGCGCATCTGCATCATCGAGCGTCC 111
QY 21 AlaAlaHisThrAlaAlaIleTyrAlaAlaArgAlaGluLeuLysProValLeuPheGlu 40
DB 112 GTTGCGCACACGGCAGCCATCTACGCGCGCGCGCGGAGCTCAGGCTGTGCTCTTCGAG 171
QY 41 GlyTyrMetAlaAsnAspIleAlaAlaGlyGlyGlnLeuThrThrThrAspValGlu 60
DB 172 GGTGATGGCAACGACATCGCGCGCGCGCGCATCTCACCACCAACCGAGCTCGAG 231
QY 61 AsnPheProGlyPheProGlyIleMetGlyValAspLeuMetAspAsnCysArgAla 80
DB 232 AACTTCCCGGGCTTCCCAACGACATCGCGCGCGCGCATCTATGACAACTGCGCGCG 291
QY 81 GlnSerLeuArgPheGlyThrAsnIleLeuSerGluThrValThrAlaValAspPheSer 100
DB 292 CAGTCCCTGGCTTTGGCAACATCTCTCCGAGACCGTCAACCGCTCGACTTTTCG 351
QY 101 AlaCysProPheArgValSerAlaAspSerThrThrValLeuAlaAspAlaValIleVal 120
DB 352 GCGTGGCCATTCGAGTTAGTCAGACTCCACACCGCTCCCGCATGCGGTATCGTT 411
QY 121 AlaThrGlyAlaValAlaArgArgLeuHisPheProGlySerAspAlaTyrTrpAsnArg 140
DB 412 GCACCGGAGCGCTCGCGCGCGCTCCACTTCCCGGGTCCCATGCACTGGAACCGC 471
QY 141 GlyIleSerAlaCysAlaValCysAspGlyAlaAlaProIlePheArgAsnLysProIle 160
DB 472 GGCATCTCCGCTGTGCGCTCTGTACGCTGCGCGCGCGCATCTCCGTAAACAGCCCATC 531
QY 161 AlaValIleGlyGlyGlyAspSerAlaMetGluGluSerAsnPheLeuThrLysTyrGly 180
DB 532 GCGCTCATAGCGCGCGCGACTCCGCTATGAGAGTCCCAATTTCTCACAAGTACGCG 591
QY 181 SerHisValTyrIleIleHisArgArgAsnThrPheArgAlaSerLysIleMetGlnAla 200
DB 592 TCCACAGTCTACATCATCCACCGCGCGCAATACCTTCGTGCTTCCAAAGATCATGCGCG 651
QY 201 ArgAlaLeuGluAsnProLysIleLysValLeuTrpAspSerGluValValGluAlaTyr 220
DB 652 AGGCGCTTGAGAAACCCAAATTAAGTCTCTTGGGACTTCGGAAGTTGTGAGGCGCTAT 711
QY 221 GlyGlyAlaAsnGlyGlyProLeuAlaGlyValLysValLysAsnLeuLeuAsnGlyGlu 240
DB 712 GCGCGCGCAACGCGCGCCATTTGGCTGGCGTAAAGGTTAAGAACCTTACTGAATGTGAG 771
QY 241 ValSerAspLeuGlnValSerGlyLeuPheAlaIleGlyHisGluProAlaThrLys 260
DB 772 GTCTCGGATCTCAGGTGTCTGGCTCTCTTCGCCATCGGGCATGAGCGCGCGCAAA 831
QY 261 PheLeuGlyGlyGlnLeuGluLeuAspSerAspGlyTyr 273
DB 832 TTCTGGGCGGACAGCTTGAATCGATTCAGATGGTTAT 870
```

RESULT 3
CK294886

LOCUS
DEFINITION

CK294886 988 bp mRNA linear EST 15-DEC-2003
EST757600 Nicotiana benthamiana mixed tissue cDNA library,
normalized, full-length Nicotiana benthamiana cDNA clone NBMCQ77 5',
end, mRNA sequence.

ACCESSION
VERSION
KEYWORDS

CK294886
CK294886.1 GI:39878724

SOURCE
ORGANISM

Nicotiana benthamiana
Nicotiana benthamiana
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiales; Solanales; Solanaceae; Nicotiana.

REFERENCE
AUTHORS

1 (bases 1 to 988)
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B.,
Staskiewicz, B., Jin, H. and Baker, B.

TITLE
JOURNAL
COMMENT

Generation of EST sequences from Nicotiana benthamiana
Unpublished (2003)
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from TIGR via potato@tigr.org
Seq primer: ATG TAG GTG ACA CTA TAG.

FEATURES
source

1..988
location/Qualifiers
/organism="Nicotiana benthamiana"
/mol_type="mRNA"
/db_xref="taxon:4100"
/clone="NBMCQ77"
/tissue_type="abiotic and biotic stress-treated leaves,
callus tissue and root tissue"
/lab_host="DH10B-TonA"
/clone_lib="Nicotiana benthamiana mixed tissue cDNA
library, normalized, full-length"
/note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
supplier: RNA was isolated from Nicotiana benthamiana
tissues that include callus, roots from liquid culture
grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
challenged leaves (Pseudomonas syringae pv tomato 12 hr;
Xanthomonas campestris pv campestris 12 hr, 18hr;
Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
campestris pv vesicatoria 18hr). RNA was isolated from
these tissues and pooled in approximately equal molar
amounts."

ORIGIN

Alignment Scores:

Pred. No.: 7,55e-136 Length: 988
Score: 1325.50 Matches: 259
Percent Similarity: 88.92% Conservative: 22
Best Local Similarity: 81.96% Mismatches: 30
Query Match: 77.56% Indels: 5
DB: 14 Gaps: 2

US-10-005-429-25 (1-331) x CK294886 (1-988)

```
QY 9 LeuArgThrArgIleCysIleIleGlySerGlyProAlaAlaHisThrAlaAlaIleTyr 28
DB 48 CTAAACACCGCGCTCTGTATCATCGCAGCGCGCGCATCATACGCCGCCATTAC 107
QY 29 AlaAlaArgAlaGluLeuLysProValLeuPheGluGlyTyrMetAlaAsnAspIleAla 48
DB 108 GCGCAGCTGCGCGAGCTGAAGCCGATCTCTTTGAAGGATGGATGGTAAACATAGCT 167
QY 49 AlaGlyGlyGlnLeuThrThrThrAspValGluAsnPheProGlyPheProAsnGly 68
DB 168 CCGCGCGGTACGATACGACCAACCGGATGCGAGAACTTTCGCCGTTTCTTGAAGT 227
QY 69 IleMetGlyAlaAspLeuMetAspAsnCysArgAlaGlnSerLeuArgPheGlyThrAsn 88
DB 228 ATTGGCGGTGGTGGAGCTTATGGACGGTCCCGTGGCAGTCCGTTCTGTTTCGGGACCAA 287
```


AUTHORS Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whiteaitt, M.S.,
 Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V. Design of
 Maize Mapping Project/DuPont Consensus Sequences for Overgo Probes
JOURNAL Unpublished (2002)
REFERENCE 2 (bases 1 to 1380)
AUTHORS Coe, E.H.
TITLE Direct Submission
JOURNAL Submitted (25-APR-2002) Maize Mapping Project, University of
 Missouri, Columbia, MO 65211, USA
COMMENT If you are interested in getting corresponding physical clones,
 these are publicly available from ZMDB and may be found by BLAST
 searching at MSL, maizemap.org; ZMDB, www.zmdb.iastate.edu; TIGR,
www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the
 maize cDNA sequences is either Virginia Walbot, Stanford or Pat
 Schnable, Iowa State, then clones may be requested from ZMDB:
www.zmdb.iastate.edu.

FEATURES Location/Qualifiers
 1..1380
 /organism="Zea mays"
 /mol_type="mRNA"
 /db_xref="maizemap:633283"
 /db_xref="taxon:4577"
 /clone_lib="Maize Mapping Project/DuPont Consensus
 Library"
 /note="this sequence is part of a project of EST
 assemblies resulting from the application of public
 contigs to seed DuPont contigs; this resource was
 assembled by DuPont as part of a collaboration for the
 overgo addressing of BACs in conjunction with the Maize
 Mapping Project"

ORIGIN

Alignment Scores:
 Pred. No.: 4,19e-178 Length: 1380
 Score: 1709.00 Matches: 331
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 11 Gaps: 0

US-10-005-429-25 (1-331) x AV104846 (1-1380)

QY 1 MetGlySerAlaAlaAlaProLeuArgThrArgGlyCysIleGlySerGlyPro 20
 DB 123 ATGGAGGGATCCGGCCGCTCCGTCGCGAGGCTGCTGCTGCTGCTGCTGCTGCT 182
 QY 21 AlaAlaHisThrAlaAlaIleTyrAlaAlaArgAlaGluLeuLeuProValLeuPheGlu 40
 DB 183 GTCTGGCACAGCGAGCCATCTACGGCGCGCGGAGCTCAAGCTGTGCTCTTCGAG 242
 QY 41 GlyTrpMetAlaAsnAspIleAlaAlaGlyGlyGlnLeuThrThrThrThrAspValGlu 60
 DB 243 GGCTGGATGGCAAGACATCCCGCGGGCGGGAGCTCACCACCACCGACGCTCGAG 302
 QY 61 AsnPheProGlyPheProAsnGlyIleMetGlyAlaAspLeuMetAspAsnCysArgAla 80
 DB 303 ACTTCCCGGGTTCCTCCCAACGGCATCATGGCGCGGAGCTCATGGACACTGCGCGG 362
 QY 81 GlnSerLeuArgPheGlyThrAsnIleLeuSerGluThrValThrAlaValAspPheSer 100
 DB 363 CAGTCCCTCGCTTTGGCACCAACATCTCTCCGAGACCGCTCACCGCGCTGACTTTTCG 422
 QY 101 AlaCysProPheArgValSerAlaAspSerThrThrValLeuAlaAspAlaValIleVal 120
 DB 423 GCTTGCCCATTCGAGTTAGTCAGACTCCACACCGTCTCGCGATGCGGTATCGTT 482
 QY 121 AlaThrGlyAlaValAlaArgArgLeuHisPheProGlySerAspAlaTyrTrpAsnArg 140
 DB 483 GCCACGGAGCGCTCGCGGGCGCTCCACTTCCCGGGTCCGATGCTACTGGAACCGC 542
 QY 141 GlyIleSerAlaCysAlaValCysAspGlyAlaAlaProIlePheArgAsnIleProIle 160

Db 543 GGCATCTCCGCTGCTGCGTCTGTGACGGTGCCTCCGCCCATCTTCCGTAAACAAGCCCATC 602
 QY 161 AlaValIleGlyGlyGlyAspSerAlaMetGluGluSerAsnPheLeuThrIleTyrGly 180
 Db 603 GCGTCTATAGCGGGCGGACTCCGCTATGAGGAGTCCAAATTTCTCCCAAGTACCGC 662
 QY 181 SerHisValTyrIleIleHisArgAsnThrPheArgAlaSerLysIleMetGlnAla 200
 Db 663 TCCACGCTCTACATCATCCACCGCGCAATACCTTCCTGCTTCCAGATCATGACGCGC 722
 QY 201 ArgAlaLeuGluAsnProLysIleValLeuTrpAspSerGluValValGluAlaTyr 220
 Db 723 AGGCGCTGTGAACCCCAAAATTAAGTCTCTCTGGGACTCGGAAGTTGTTCGAGCCCTAT 782
 QY 221 GlyGlyAlaAsnGlyGlyProLeuAlaGlyValLysValLysAsnLeuLeuAsnGlyGlu 240
 Db 783 GCGCGCGCAACCGCGCGCCCATTCGCTGGCTAAGGTTAAGACCTACTGATGGTGAG 842
 QY 241 ValSerAspLeuGlnValSerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLys 260
 Db 843 GTCTCGCATCTTCAAGTGTCTGCGCTCTTCTTCGCCATCGGCGCATGAGCGCGGACCAA 902
 QY 261 PheLeuGlyGlyGlnLeuGluLeuAspSerAspGlyTyrValGluThrLysProGlySer 280
 Db 903 TTCTGGCGGACAGCTTGAATCTGATTCAGATGGTTATGTGGAAACCAAGCCAGGTTC 962
 QY 281 ThrHisThrSerValLysGlyValPheAlaAlaGlyAspValGlnAspLysIleTyrArg 300
 Db 963 ACTCACACCACTGTAAAGGGTGTATTTGCTCTCGCGACGTGCGAGCAACAGAGTACCGT 1022
 QY 301 GlnAlaIleThrAlaAlaGlySerGlyCysMetAlaAlaLeuAspAlaGluHisTyrLeu 320
 Db 1023 CAGGCCATTACTGCGCTGGATCGGGTGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1082
 QY 321 GlnGluIleGlyAlaGlnGluGlyLysSerAsp 331
 Db 1083 CAGGAGATCGGTGCGACAGGAGGAAAGTCTCAT 1115

RESULT 2
 CG300268
 LOCUS
 DEFINITION OG2AE91TV ZM.0.7.1.5 KB Zea mays genomic clone ZMMBma0742013,
 genomic survey sequence.
 ACCESSION CG300268
 VERSION CG300268.1 GI:34214482
 KEYWORDS GSS.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 REFERENCE 1 (bases 1 to 871)
 AUTHORS Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
 Resnick, A., Frazer, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
 Citek, R.W., Numborg, A., Robbins, D. and Lakey, N.
 Consortium for Maize Genomics
 Unpublished (2002)
 JOURNAL Other GSSs: OG2AE91TH
 COMMENT Contact: Cathy Whitelaw
 TIGR
 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301-838-5843
 Fax: 301-838-0208
 Email: whitelaw@tigr.org
 Seq primer: Tg
 Class: sheared ends
 FEATURES Location/Qualifiers
 1..871
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /strain="B73"
 /db_xref="taxon:4577"
 /clone="ZMMBma0742013"

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 5, 2004, 03:03:23 ; Search time 3070.26 Seconds
(without alignments)
3219.395 Million cell updates/sec

Title: US-10-005-429-25
Perfect score: 1709
Sequence: 1 MEGSAAPLRICIGSGP.....AALDAHYLQETGAQEGKSD 331

Scoring table:
BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DRV=xlp
-O=/cgn2.1/USPTO.spool.p/US10005429/runat_04052004_121649_15445/app_query.fasta_1.782
-DB=EST -OFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pcr -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10005429 @CEN_1_1_5436 @runat_04052004_121649_15445 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DRV TIMEOUT=120 -WARM TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estm:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hcc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hcc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_man:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rtd:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*

29: gb_gss2:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match %	Length	DB	ID	Description
1	1709	100.0	1380	11	AY104846	AY104846 Zea mays
2	1412	82.6	871	29	CG300268	CG300268 OGA2AE91TV
3	1325.5	77.6	988	14	CK294886	CK294886 EST757600
4	1324.5	77.5	946	14	CK292570	CK292570 EST755284
5	1304.5	76.3	981	14	CK283459	CK283459 EST746181
6	1262.5	74.2	976	14	CK289722	CK289722 EST752444
7	1262.5	73.9	970	14	CK278585	CK278585 EST724663
8	1255.5	73.5	947	14	CK286466	CK286466 EST749188
9	1251.5	73.2	993	14	CK250238	CK250238 EST733875
10	1239.5	72.5	946	14	CK258706	CK258706 EST742343
11	1235.5	72.3	943	14	CK252016	CK252016 EST735653
12	1222.5	71.5	930	14	CK289221	CK289221 EST751943
13	1206.5	70.6	981	14	CK270016	CK270016 EST716094
14	1202.5	70.4	920	14	CK280506	CK280506 EST743228
15	1202.5	70.4	995	14	CK255109	CK255109 EST738746
16	1200.5	70.2	933	14	CK298849	CK298849 EST761563
17	1198.5	70.1	958	14	CK245751	CK245751 EST729388
18	1198.5	70.1	962	14	CK257667	CK257667 EST741304
19	1191.5	69.7	927	14	CK296353	CK296353 EST759067
20	1191.5	69.7	937	14	CK265799	CK265799 EST711877
21	1184.5	69.3	950	14	CK255628	CK255628 EST739265
22	1183.5	69.3	934	14	CK296331	CK296331 EST759045
23	1181.5	69.1	897	14	CK246992	CK246992 EST730829
24	1176.5	68.8	910	14	CK285686	CK285686 EST748408
25	1156.5	67.7	935	14	CK254145	CK254145 EST737782
26	1151.5	67.4	968	14	CK243644	CK243644 EST727281
27	1150.5	67.3	901	14	CK296358	CK296358 EST759072
28	1144.5	67.0	908	14	CK298635	CK298635 EST761349
29	1143.5	66.9	907	14	CK280632	CK280632 EST743354
30	1136	66.5	783	14	CB673195	CB673195 OSUNE007J
31	1135	66.4	729	14	CD881998	CD881998 F1.104P10
32	1130.5	66.1	915	14	CK254872	CK254872 EST738509
33	1128.5	66.0	924	14	CK244678	CK244678 EST728315
34	1127.5	66.0	891	14	CK288120	CK288120 EST750842
35	1125.5	65.9	874	14	CK291485	CK291485 EST754199
36	1119.5	65.5	950	14	CK274289	CK274289 EST720367
37	1118.5	65.4	968	14	CK258564	CK258564 EST742201
38	1116.5	65.3	893	14	CK284817	CK284817 EST747539
39	1114.5	65.2	982	14	CK296140	CK296140 EST758854
40	1112	65.1	958	11	AY105128	AY105128 Zea mays
41	1109.5	64.9	854	14	CK291401	CK291401 EST754115
42	1104.5	64.6	929	14	CK253514	CK253514 EST737151
43	1102.5	64.5	955	14	CK290438	CK290438 EST753152
44	1098.5	64.3	841	14	CK297625	CK297625 EST760339
45	1097	64.2	861	14	CB643663	CB643663 OSUNE004H

ALIGNMENTS

RESULT 1
AY104846
LOCUS Zea mays
DEFINITION Zea mays P00061833 mRNA sequence.
ACCESSION AY104846
VERSION AY104846.1 GI:21207924
KEYWORDS HTC.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 1380) linear mRNA HTC 16-OCT-2002

CC a first sequence to regulate transcription, a second DNA sequence
 CC encoding a fusion polypeptide, comprising a sequence encoding an oleosin
 CC gene and sequence encoding (i) and a third sequence encoding a
 CC termination region functional in the host cell and growing the host cell
 CC to produce a fusion polypeptide. The method or (i) is useful for
 CC expression of a thioridoxin or thioridoxin reductase by a host cell. This
 CC sequence encodes Arabidopsis thaliana thioridoxin reductase
 XX
 SQ Sequence 3787 BP; 1221 A; 677 C; 621 G; 1268 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 3,91e-126 Length: 3787
 Score: 1318.00 Matches: 254
 Percent Similarity: 86.77% Conservativity: 28
 Best Local Similarity: 78.15% Mismatches: 39
 Query Match: 77.12% Indels: 4
 Gaps: 6
 DB: 1

US_10-005-429-25 (1-331) x ABS53098 (1-3787)

QY 11 ThrArgileCysilelleGlySerGlyProAlaAlaHisThrAlaAlaIleTyrAlaAla 30
 DB 1579 ACAAGGCTCTGTATCGTAGGAGTGGCCACACGCGCGCGATTACGCGAGCT 1638
 QY 31 ArgAlaGluLeuLysProValLeuPheGluGlyTyrMetAlaAsnAspIleAlaGly 50
 DB 1639 AGGGCTGAACCTTAACCTCTCTTCGAGGAGTGGATGGCTAACGACATCGCTCCCGGT 1698
 QY 51 GlyGlnLeuThrThrThrAspValGluAsnPheProGlyPheProAsnGlyIleMet 70
 DB 1699 GGTCACCTAACCAACACCGAGCTGAGAAATTTCCCGGATTTCCAGAGGATTTCTC 1758
 QY 71 GlyAlaAspLeuMetAspAsnCysArgAlaGlnSerLeuArgPheGlyThrAsnIleLeu 90
 DB 1759 GGAGTAGAGCTCACTGACAAATTCGGTAAACATCGGAGCGATTCGGTACTACGATTT 1818
 QY 91 SerGluThrValThrAlaValAspPheSerAlaCysProPheArgValSerAlaAspSer 110
 DB 1819 ACAGAGACGGTGACGAAGTGGATTCTCTCGAACCCTTTAAGCTATTTCACAGATTCA 1878
 QY 131 ThrThrValLeuAlaAspAlaValIleValAlaThrGlyAlaValAlaArgArgLeuHis 130
 DB 1879 AAAGCCATTCTCGCTGACGCTGTGATTCGCTACTGGAGCTGTGGCTAAGCGGCTTAGC 1938
 QY 131 Phe-----ProGlySerAspAlaTyrTrpAsnArgGlyIleSerAlaCysAla 146
 DB 1939 TTGGTGGATCTGGTGAAGTTCTGGAGGTTCTTGGAACCGTGAAATCTCCGCTTGCT 1998
 QY 147 ValCysAspGlyAlaAlaProIlePheArgAsnLysProIleAlaValIleGlyGly 166
 DB 1999 GTTTGGACGGAGCTGCTCGATATTCGTAACAACTCTTCGGGTGATCGGTGGAGGC 2058
 QY 167 AspSerAlaMetGluGluSerAsnPheLeuThrIleTyrGlySerHisValTyrIleIle 186
 DB 2059 GATTACGAAATGGAAGAACAACTTCTTACAAATATGGAATCTAAAGTGTATATAATC 2118
 QY 187 HisArgArgAsnThrPheArgAlaSerIleMetGlnAlaLeuGluAsnPro 206
 DB 2119 CATAGAGAGATCTTTAGAGGCTCTAAGATTATGACGAGCGAGCTTTGTCTAATCT 2178
 QY 207 LysIleLysValLeuTrpAspSerGluValGluAlaTyrGlyAlaAsnGlyGly 226
 DB 2179 AAGATTGATGTGATTTGGAATCTGCTGTGTGTGGAAGCTTTATGGAGATGGAGAAAGAT 2238
 QY 227 ProLeuAlaGlyValLysValLysAsnLeuAsnGlyGluValSerAspLeuGlnVal 246
 DB 2239 GTGCTTGGAGATTTGAAGTGAAGATGTGGTTACCGGAGATGTTCTGATTTAAAGTT 2298
 QY 247 SerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLysPheLeuGlyGlnLeu 266
 DB 2299 TCTGGATTGTTCTTTGCTATTTGCTATGCTAGCCAGCTACCAAGTTTTCGATGCTGTT 2358
 QY 267 GluLeuAspSerAspGlyTyrValGluThrLysProGlySerThrHisThrSerValLys 286

DB 2359 GAGTTAGATTGGATGGTTATGTTGTACGAGCCTGGTACTACACAGACTAGCGTTCCC 2418
 QY 287 GlyValPheAlaAlaGlyAspValGlnAspLysLysTyrArgGlnAlaIleThrAlaAla 306
 DB 2419 GGAGTTTTCGCTGCGGTGATGTTTCAAGATAGAAGTATAGGCAAGCCATCACTGCTGCA 2478
 QY 307 GlySerGlyCysMetAlaAlaLeuAspAlaGluHisTyrLeuGlnGluIleGlyAlaGln 326
 DB 2479 GGAACCTGGGTGCATGCGAGCTTTGGATGCGAGCATTACTTACAAGAGATTGGATCTCAG 2538
 QY 327 GluGlyLysSerAsp 331
 DB 2539 CAAGGTAAAGATGAT 2553

Search completed: May 5, 2004, 03:24:26
 Job time : 437.882 secs

recombinant polypeptide (P1, P2), where P1 is capable of associating with P2 to form the MPC and associating the complex with an occlusion body (OB) through an OB-targeting-protein capable of associating with OB and P1. M1 is useful for producing an oil body associated with a recombinant MPC. The oil bodies are further formulated for use in the preparation of a food product such as milk or wheat based food product, personal care product which reduces the oxidative stress on the surface area of the human body or used to lighten the skin, or a pharmaceutical composition used to treat chronic obstructive pulmonary disease (COPD), cataracts, diabetes, envenomation, bronchiopulmonary disease, psoriasis, malignancies, reperfusion injury, wound healing, sepsis, gastro intestinal (GI) bleeding, intestinal bowel disease (IBD), ulcers, GERD (gastro oesophageal reflux disease). ABN89569 to ABN9593 and ABP0677 to CC ABP60364 represent sequence given in the exemplification of the present invention

SQ Sequence 3787 BP; 1221 A; 577 C; 621 G; 1268 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 3.91e-136 Length: 3787
Score: 1318.00 Matches: 254
Percent Similarity: 86.77% Conservative: 28
Best Local Similarity: 78.15% Mismatches: 39
Query Match: 77.12% Indels: 4
Gaps: 1

US-10-005-429-25 (1-331) x ABN89582 (1-3787)

Qy 11 ThrArgIleCysIleIleGlySerGlyProAlaAlaHisThrAlaAlaIleThrAlaAla 30
Db 1579 ACAGGCTCTGTATCGTAGGAGTGGCCGCGGCGCACACGCGCGGCGATTACGAGCT 1638
Qy 31 ArgAlaGluLeuLysProValLeuPheGluGlyTrpMetAlaAsnAspIleAlaAlaGly 50
Db 1639 AGGGCTGAATTAACCTCTCTCTCGAAGGATGGATGGCTAACGACATCGCTCCCGGT 1698
Qy 51 GlyGlnLeuThrThrThrAspValGluAsnPheProGlyPheProAsnGlyIleMet 70
Db 1699 GGTCACTTACACACACCGAGCTCGAGATTTCCCGGATTTCCAGAGGTATCTC 1758
Qy 71 GlyAlaAspLeuMetAspAsnCysArgAlaGlnSerLeuArgPheGlyThrAsnIleLeu 90
Db 1759 GGAGTAGAGCTCAGTACAAATTCGTAACAAATTCGAGCGGATTCGGTACTACGATATT 1818
Qy 91 SerGluThrValThrAlaValAspPheSerAlaCysProPheArgValSerAlaAspSer 110
Db 1819 ACAGAGCGGTACGAAAGTGGATTTCTTTCGAAACCGTTTACGCTATTACAGATTCA 1878
Qy 111 ThrThrValLeuAlaAspAlaValIleValAlaThrGlyAlaValAlaArgGlyLeuHis 130
Db 1879 AAAGCATTCCTCGCTGACGCTGTGATTCTCGCTACTGCGAGCTGTGGCTAAGCGGCTTAGC 1938
Qy 131 Phe-----ProGlySerAspAlaTyrrTrpAsnArgGlyIleSerAlaCysAla 146
Db 1939 TTCGTTGGATCTGGTGAAGTTCTCGAGTTTCTGGAACCGTGGAAATCTCCGCTGTGCT 1998
Qy 147 ValCysAspGlyValAlaAlaProIlePheArgAsnLysProIleAlaValIleGlyGlyGly 166
Db 1999 GTTTCGAGCGAGCTGCTCCGATATTCGTAACAACTCTTGGCTGTGATCGGTGAGGAC 2058
Qy 167 AspSerAlaMetGluSerAsnPheLeuThrLysTyrrGlySerHisValTyrrIleIle 186
Db 2059 GATTTCAGCAATGGAAGAAGCAACTTCTTACAAAATATGGATCTTAAAGTGTATATAATC 2118
Qy 187 HisA-GATGATPheArgAlaSerLysIleMetGlnAlaArgAlaLeuGluAsnPro 206
Db 2119 CATGAGAGATGCTTTTAGAGCGTCTAAGATTATGCGACGCGAGCTTTGTCTAATCT 2178
Qy 207 LysIleLysValLeuTrpAspSerGluValValGluAlaTyrrGlyAlaAsnGlyGly 226
Db 2179 AAGATTGATGATTGGAACTCGTCTGTTGTGGAAGCTTATGGAGATGGAGAAAGAT 2238
Qy 227 ProLeuAlaGlyValLysValLysAsnLeuAsnGlyGluValSerAspLeuGlnVal 246

Db 2239 GTGCTGGAGGATTGAAGTGAAGAATGTGGTTACCGGAGATGTTCTGATTTAAAAGTT 2298
Qy 247 SerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLysPheLeuGlyGlyGlnLeu 266
Db 2299 TCTGGATTGTTCTTCTGATGTCTATGTCTATGAGCCAGCTACCAAGTTTGGATGGTGT 2358
Qy 267 GluLeuAspSerAspGlyTyrrValGluThrLysProGlySerThrHisThrSerValLys 286
Db 2359 GAGTAGATTGGGATGGTATGTTGTACCAAGCCTGGTACTACACAGACTAGCGTTCC 2418
Qy 287 GlyValPheAlaAlaGlyAspValGlnAspLysLysTyrrArgGlnAlaIleThrAlaAla 306
Db 2419 GAGATTTCCTCGCGGTGATGTCTAGGATPAGAGATPAGGAGCCATCCTGCTGCA 2478
Qy 307 GlySerGlyCysMetAlaAlaLeuAspAlaGluHisTyrrLeuGlnIleGlyAlaGln 326
Db 2479 GGAACCTGGGTGCATGGCAGCTTTGGATGCAGAGCATTTACTTACAGAGATTGGATCTCAG 2538
Qy 327 GluGlyLysSerAsp 331
Db 2539 CARGTAAGAGTGTAT 2553
RESULT 15
ABSS3098
ID ABSS3098 standard; cDNA; 3787 BP.
XX AC ABSS3098;
XX DT 29-NOV-2002 (first entry)
XX DE cDNA encoding Arabidopsis thioredoxin reductase.
XX KW Thioredoxin; thioredoxin reductase; gene expression; oleosin; oil body;
XX KW oleosin-Chioredoxin fusion protein; Gene; ss.
XX OS Arabidopsis thaliana.
XX FH Key Location/Qualifiers
XX CDS 1555..2550
XX FT /*tag= a
XX FT /product= "Thioredoxin reductase"
XX PN US2002088025-A1.
XX PD 04-JUL-2002.
XX PF 03-JUL-2001; 2001US-00897425.
XX PR 22-FEB-1991; 91US-00659835.
XX PR 16-NOV-1993; 93US-00142418.
XX PR 30-DEC-1994; 94US-00366783.
XX PR 25-APR-1997; 97US-00846021.
XX PR 18-DEC-1998; 98US-00210843.
XX PA (MOLO/) MOLONEY M M.
XX PA (DALM/) DALMIA B K.
XX PI Moloney MM, Dalmia BK;
XX DR WPI; 2002-635723/68.
XX DR P-FSDB; ABG32921.
XX PT Expressing protein, by introducing chimeric nucleotide regulatory
XX PT sequence, sequence encoding fusion protein, having sequence encoding
XX PT protein, oleosin gene and sequence encoding termination region and
XX PT producing protein.
XX PS Example 21; Fig 15; 69pp; English.
XX CC The invention describes a method of expressing thioredoxin or thioredoxin
XX CC reductase (I) in the oil body of a host cell using an oil body protein
XX CC gene. The method involves introducing a chimeric nucleic acid comprising

PR 21-OCT-1999; 99US-0160770P.
 PR 21-OCT-1999; 99US-0160814P.
 PR 21-OCT-1999; 99US-0160815P.
 PR 22-OCT-1999; 99US-0160980P.
 PR 22-OCT-1999; 99US-0160981P.
 PR 22-OCT-1999; 99US-0160989P.
 PR 25-OCT-1999; 99US-0161404P.
 PR 25-OCT-1999; 99US-0161405P.
 PR 25-OCT-1999; 99US-0161406P.
 PR 26-OCT-1999; 99US-0161359P.
 PR 26-OCT-1999; 99US-0161360P.
 PR 26-OCT-1999; 99US-0161361P.
 PR 28-OCT-1999; 99US-0161920P.
 PR 28-OCT-1999; 99US-0161922P.
 PR 28-OCT-1999; 99US-0161933P.
 PR 29-OCT-1999; 99US-0162142P.

Alignment Scores:
 Pred. No.: 1.15e-126 Length: 1539
 Score: 1318.00 Matches: 254
 Percent Similarity: 86.77% Conservative: 28
 Best Local Similarity: 78.15% Mismatches: 39
 Query Match: 77.12% Indels: 4
 DB: 3 Gaps: 1

US-10-005-429-25 (1-331) x AAC36511 (1-1539)

QY 11 ThrArgIleCysIleIleGlySerGlyProAlaAlaHisThrAlaAlaIleTyrAlaAla 30
 DB 236 ACAAGGCTCTGTATCGTAGAGAGTGGCCCGGACACACACCGCGGATTTACGCGAGCT 295

QY 31 ArgAlaGluLeuLysProValLeuPheGluGlyTyrMetAlaAsnAspIleAlaAlaGly 50
 DB 296 AGGGCTGAACCTTAACCTCTCTTCGAAAGGATGGATGCTAACGACATCGCTCCCGGT 355

QY 52 GlyGlnIleuThrThrThrAspValGluAsnPheProGlyPheProAsnGlyIleMet 70
 DB 356 GGTCACTAACACACACCGACGTCGAGAAATTCGCCGGATTTCCAGAGGATTTCTC 415

QY 71 GlyAlaAspLeuMetAspAsnCysArgAlaGlnSerLeuArgPheGlyThrAsnIleLeu 90
 DB 416 GGAATAGAGCTCACTGACAAATTCGGTAACATCGGAGCGATTCGGTACTAGATATT 475

QY 91 SerGluThrValThrAlaValAspPheSerAlaCysProPheArgValSerAlaAspSer 110
 DB 476 ACAGACGCGTGACGAAGTCGATTTCTCTCGAAACCGGTTTAAGCTATTTCACAGATCA 535

QY 111 ThrThrValLeuAlaAspAlaValIleValAlaThrGlyValAlaAlaArgArgLeuHis 130
 DB 536 AAGCCATTCCTGCTGACGCTGTGATTCCTGCTACTGAGCTGTGGCTAAGCGGCTTAGC 595

QY 131 Phe-----ProGlySerAspAlaTyrTyrAsnArgGlyIleSerAlaCysAla 146
 DB 596 TCGTTGGATCTGGTGAAGGTTCTGGAGGTTCTGGAAACCGTGGAAATCTCGGCTTGCT 655

QY 147 ValCysAspGlyAlaAlaProIlePheArgAsnLysProIleAlaValIleGlyGlyGly 166
 DB 656 GTTTGGAGCGAGCTGCTCGATTTCCGTACAAACCTTCCTCGGTGATCGGTGAGGC 715

QY 167 AspSerAlaMetGluGluSerAsnPheLeuThrLysTyrGlySerHisValTyrIleIle 186
 DB 716 GATTGAGCAATGGAAGAAGCAAACTTCTTACAAATATGGATCTAAAGTGATATAATC 775

QY 187 HisArgArgAsnThrPheArgAlaSerLysIleMetGlnAlaArgAlaLeuGluAsnPro 206
 DB 776 CATAGAGAGATGCTTTTAGGGCTTAAGATTATCGACGAGCTTTGCTTAATCT 835

QY 207 LysIleLysValLeuThrAspSerGluValValGluAlaTyrGlyAlaAsnGlyGly 226
 DB 836 AAGATTGATGATTGGAACTCGTCTGTGTGGAAGCTTATGGAGATGGAAGAAGAT 895

QY 227 ProLeuAlaGlyValLysValLysAsnLeuLeuAsnGlyGluValSerAspLeuVal 246

Db 896 GTCTTGGAGGATTGAAGTGAAGAAATGTGGTTTACCGGAGATGTTTCTGATTTAAAGTT 955

Qy 247 SerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLysPheLeuGlyGlnLeu 266
 Db 956 TCTGGATTGTTCTTCTGTTATGTCATGAGCCAGCTACCAAGTTTTCGATGGTGGTT 1015

Qy 267 GluLeuAspSerAspGlyTyrValGluThrLysProGlySerThrHisThrSerValLys 286
 Db 1016 GAGTTAGATTCCGATGTTATGTTGTCAGAAAGCTGGTACTACAGACTACGCTTCCC 1075

Qy 287 GlyValPheAlaAlaGlyAspValGlnAspLysLysTyrArgGlnAlaIleThrAlaAla 306
 Db 1076 GGAATTTTCGCTCGCGGTGATGTTTCAGGATAGAAGTATAGCAAGCCATCATCTGCTCA 1135

Qy 307 GlySerGlyCysMetAlaAlaLeuAspAlaGluHisTyrLeuGlnGluLeuGlyAlaGln 326
 Db 1136 GGAACCTGGGTGATGCGAGCTTTGGATGCGAGCATTACTTACAGAGATTGGATCTCAG 1195

Qy 327 GluGlyLysSerAsp 331

Db 1196 CAGGTAAGATGAT 1210

RESULT 14
 ABN89582
 ID ABN89582 standard; DNA; 3787 BP.
 XX
 AC ABN89582;
 XX
 DT 06-SEP-2002 (first entry)
 XX
 DE Phaseolin promoter-thioredoxin reductase-phaseolin terminator DNA #22.
 XX
 KW Multimeric protein; redox protein; thioredoxin; thioredoxin reductase;
 KW oil body; ophthalmological; antidiabetic; cytotaxtic; antiposoriatic;
 KW vasotropic; vulnary; antibacterial; immunosuppressive; antitumor;
 KW food product; milk; wheat; oxidative stress; cataract; diabetes;
 KW chronic obstructive pulmonary disease; envenomation; psoriasis; sepsis;
 KW bronchiopulmonary disease; malignancy; reperfusion injury; wound healing;
 KW gastro intestinal bleeding; intestinal bowel disease; ulcer;
 KW gastro oesophageal reflux disease; gene; ds.
 XX
 OS Arabidopsis sp.
 OS Phaseolus vulgaris.
 XX
 PN W0200250289-A1.
 XX
 PD 27-JUN-2002.
 XX
 PF 19-DEC-2001; 2001WO-US050240.
 XX
 PR 19-DEC-2000; 2000US-00742900.
 PR 05-JUL-2001; 2001US-0302885P.
 PR 04-DEC-2001; 2001US-00006038.
 XX
 PA (SEMB-) SEMBIOSYS GENETICS INC.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 XX
 PI Van Rooijen G, Deckers H, Heifetz PS, Briggs SP, Dalmia BK,
 PI Del Val G, Zaplachinski S, Moloney M;
 XX
 DR WPI: 2002-508806/54.
 DR P-PSDB; ABP60685.
 XX
 PT Producing oil body associated with recombinant multimeric protein complex
 PT e.g. redox proteins and immunoglobulins comprises producing recombinant
 PT polypeptides capable of forming the complex in cells comprising oil
 PT bodies.
 XX
 PS Example 2; Page 173-175; 362pp; English.
 XX
 CC The present invention describes a method (M1) for producing an oil body
 CC associated with a recombinant multimeric protein complex (MPC). M1
 CC comprises producing in a cell comprising oil bodies a first and second

[illegible]

```

PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159325P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Alignment Scores:
Pred. No.: 1,05e-126 Length: 1438
Score: 1318.00 Matches: 254
Percent Similarity: 86.77% Conservative: 28
Best Local Similarity: 78.15% Mismatches: 39
Query Match: 77.12% Indels: 4
DB: 3 Gaps: 1

US-10-005-429-25 (1-331) x AAC38830 (1-1438)

Qy 11 ThrArgIleCysIleIleGlySerGlyProAlaAlaHisThrAlaAlaIleTyrAlaAla 30
Db 135 ACAAGGCTCTGTATCGTAGGAGTGGCCAGGCGCACACAGCGGGCGGATTTACGAGCT 194

Qy 31 ArgAlaGluLeuLysProValLeuPheGluGlyTrpMetAlaAenAspIleAlaAlaGly 50
Db 195 AGGCTGAACCTAAACCTCTTCTCTCGAAGATGATGGTACGACATCGCTCCCGGT 254

Qy 51 GlyGlnLeuThrThrThrAspValGluAsnPheProGlyPheProAsnGlyIleMet 70
Db 255 GGTCACTTAACACACACACCGAGCTCGAGATTTCCCGGATTTCCAGAGGATTTCTC 314

Qy 71 GlyAlaAspLeuMetAspAsnCysArgAlaGlnSerLeuArgPheGlyThrAsnIleLeu 90
Db 315 GGAGTAGAGCTCACTGACAAATTCGGTAAACATCGGAGCGATTCGGTACTACGATATT 374

Qy 91 SerGluThrValThrAlaValAspPheSerAlaCysProPheArgValSerAlaAspSer 110
Db 375 ACAGAGCGGTGACGAAGTCGATTTCTCTCTGAAACCGTTTAAGCTATTACACAGATTCA 434

Qy 111 ThrThrValLeuAlaAspAlaValIleValAlaThrGlyAlaValAlaArgArgLeuHis 130
Db 435 AAGCCATCTCGCTGACGCTGTGATTTCTGCTACTGAGACTGTGGCTTAGCGGCTTAGC 494

Qy 131 Phe-----ProGlySerAspAlaTyrTrpAsnArgGlyIleSerAlaCysAla 146
Db 495 TTCGTTGGATCTGGTGAAGGTTCTGGAGGTTCTCGAACCCTGGAATCTCCGCTTGCT 554

Qy 147 ValCysAspGlyAlaAlaProIlePheArgAsnLysProIleAlaValIleGlyGly 166
Db 555 GTTTCGACGAGCTGCTCGATATTCGTAACAAACCTCTTGGGATCGGTGGAGGC 614

Qy 167 AspSerAlaMetGluSerAsnPheLeuThrLysTyrGlySerHisValTyrIle 186
Db 615 GATTCAGCAATGGAAGCAAACTTTCTTACAAATATGATCTAAAGTGATATAATC 674

187 HisArgArgAsnThrPheArgAlaSerLysIleMetGlnAlaArgAlaLeuGluAsnPro 206
675 CATAGAGAGAGATGCTTTACAGCGCTCTAAGATTATGACGACGAGCTTTGTCTAATCT 734

207 LysIleLysValLeuTrpAspSerGluValValGluAlaTyrGlyGlyAlaAsnGlyGly 226
735 AAGATTGATGATTTGGAATCTGCTCTGTTGTGGAAGCTTATGGAGATGGAGAAAGAGAT 794

227 ProLeuAlaGlyValLysValLysAsnLeuLeuAsnGlyGluValSerAspLeuGlnVal 246
795 GTGCTTGGAGATGAAAGTGAAGATGCTGTTACCGGAGATGTTTCTGATTTAAAGATT 854

247 SerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLysPheLeuGlyGlyGlnLeu 266
855 TCTGGATTGTCTTCTGATTGCTATGCTAGCCAGCTACCAAGTTTGTGGATGGTGGTGT 914

267 GluLeuAspSerAspGlyTyrValGluThrLysProGlySerThrHisThrSerValLys 286
915 GAGTTAGATTCGATGCTGTTGTTGTCACGAGCCTGGTACTACACAGACTAGGTTCCC 974

287 GlyValPheAlaAlaGlyAspValGlnAspLysLysTyrArgGlnAlaIleThrAlaAla 306
975 GGAGTTTTCGCTCGGCTGATGTTTACGATTAAGATATAGGCAAGCCATCCTGCTGCA 1034

307 GlySerGlyCysMetAlaAlaLeuAspAlaGluHisTyrLeuGlnGluIleGlyAlaGln 326
1035 GGAACCTGGGTCATGGCAGCTTTGGATGACAGACATTACTTACAGAGATTGGATCTCAG 1094

327 GluGlyLysSerAsp 331
1095 CAAGGTAAGATGAT 1109

RESULT 13
AAC36511
ID AAC36511 standard; DNA; 1539 BP.
XX
AC AAC36511;
DT
XX 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 14081.
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000BP-00301439.
XX
PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-01233548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 25-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 23-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.

```


Fri May 7 13:26:58 2004

PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 23-APR-1999; 99US-0130691P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 06-MAY-1999; 99US-0132487P.
PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 18-MAY-1999; 99US-0134941P.
PR 19-MAY-1999; 99US-0135124P.
PR 20-MAY-1999; 99US-0135353P.
PR 21-MAY-1999; 99US-0135629P.
PR 24-MAY-1999; 99US-0136021P.
PR 25-MAY-1999; 99US-0136392P.
PR 27-MAY-1999; 99US-0136782P.
PR 28-MAY-1999; 99US-0137222P.
PR 01-JUN-1999; 99US-0137528P.
PR 03-JUN-1999; 99US-0137502P.
PR 04-JUN-1999; 99US-0137724P.
PR 07-JUN-1999; 99US-0138094P.
PR 08-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 10-JUN-1999; 99US-0139119P.
PR 14-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 16-JUN-1999; 99US-0139492P.
PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 05-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 06-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 09-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149923P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154048P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158365P.
PR 13-OCT-1999; 99US-0159293P.

OS Arabidopsis sp.
 XX W0200250289-A1.
 PN 27-JUN-2002.
 XX 19-DEC-2001; 2001WO-US050240.
 XX 19-DEC-2000; 2000US-00742900.
 PR 05-JUL-2001; 2001US-0302885P.
 PR 04-DEC-2001; 2001US-00006038.
 XX (SEMB-) SEMBIOSYS GENETICS INC.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 XX Van Rooijen G, Deckers H, Heifetz PB, Briggs SP, Dalmia BK;
 PI Del Val G, Zaplachinski S, Moloney M;
 PI MPI; 2002-508906/54.
 XX Producing oil body associated with recombinant multimeric protein complex
 PT e.g. redox proteins and immunoglobulins comprises producing recombinant
 PT polypeptides capable of forming the complex in cells comprising oil
 PT bodies.
 XX Claim 68; Page 161-162; 362pp; English.
 XX The present invention describes a method (M1) for producing an oil body
 CC associated with a recombinant multimeric protein complex (MPC). M1
 CC comprises producing in a cell comprising oil bodies a first and second
 CC recombinant polypeptide (P1, P2), where P1 is capable of associating with
 CC P2 to form the MPC and associating the complex with an occlusion body
 CC (OB) through an OB-targeting-protein capable of associating with OB and
 CC P1. M1 is useful for producing an oil body associated with a recombinant
 CC MPC. The oil bodies are further formulated for use in the preparation of
 CC a food product such as milk or wheat based food product, personal care
 CC product which reduces the oxidative stress on the surface area of the
 CC human body or used to lighten the skin, or a pharmaceutical composition
 CC used to treat chronic obstructive pulmonary disease (COPD); cataracts,
 CC diabetes, emphysema, bronchiopulmonary disease, psoriasis,
 CC malignancies, reperfusion injury, wound healing, sepsis, gastro
 CC intestinal (GI) bleeding, intestinal bowel disease (IBD), ulcers, GERD
 CC (gastro oesophageal reflux disease). ABN89569 to ABN89593 and ABP60677 to
 CC ABP60964 represent sequence given in the exemplification of the present
 CC invention
 XX SQ Sequence 1002 BP; 259 A; 196 C; 272 G; 275 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 6.39e-127 Length: 1002
 Score: 1318.00 Matches: 254
 Percent Similarity: 86.77% Conservative: 28
 Best Local Similarity: 78.15% Mismatches: 39
 Query Match: 77.12% Indels: 4
 DB: 6 Gaps: 1

US-10-005-429-25 (1-331) x ABN89578 (1-1002)

QY 11 ThrArgIleCysIleIleGlySerGlyProAlaAlaHisThrAlaAlaIleTyrAlaAa 30
 DB 25 ACAAGGCTCTGTATCGTAGGAAGTGGCCGCGGACACACGCGCGGATTTACGAGCT 84
 QY 31 ArgAlaGluLeuLysProValLeuPheGluGlyTyrMetAlaAsnAspIleAlaAaGly 50
 DB 85 AGGGTGAACTTAACCTCTCTCTTCAAGGATGGATGCTAACGACATCGTCCCGGT 144
 QY 51 GlyGlnLeuThrThrThrAspValGluAsnPheProGlyPheProAsnGlyIleMet 70
 DB 145 GGTCACTAAACACACCGGCTGAGATTTCCCGGATTTCCAGAGGTATTTCTC 204
 QY 71 GlyAlaAspLeuMetAspAsnCysArgAlaGlnSerLeuArgPheGlyThrAsnIleLeu 90
 DB 205 GGAGTAGAGTCACTGACAAATCCGTAAACATCGGAGGATTCGTACTACGATATT 264

QY 91 SerGluThrValThrAlaValAspPheSerAlaCysProPheArgValSerAlaAspSer 110
 DB 265 ACAGAGACGGTGCAGAAAGTCGATTCTCTCGAAACCGTTTAAAGCTATTTCAGATTCA 324
 QY 111 ThrThrValLeuAlaAspAlaValIleValAlaThrGlyAlaValAlaArgGluHis 130
 DB 325 AAAGCCATTCTCGCTGACGCTGTGATTCGCTACTGGAGCTGTGGCTAAGCGGCTTAGC 384
 QY 131 Phe-----ProGlySerAspAlaTyrTrpAsnArgGlyIleSerAlaCysAla 146
 DB 385 TTGCTGGATCTGGTGAAGCTTCTGGAACCGTGGAAATCTCCGCTTGCT 444
 QY 147 ValCysAspGlyAlaAlaProIlePheArgAsnLysProIleAlaValIleGlyGly 166
 DB 445 GTTTCGACGGAGCTGCTCCGATATTCGGTAACAACTCTTCGCGTGATTCGGTGGAGC 504
 QY 167 AspSerAlaMetGluGluSerAsnPheLeuThrLysTyrGlySerHisValTyrIleIle 186
 DB 505 GATTCAGCANTGGAGACCAACTTCTTACAAATATGATGATCTAAAGTGTATATATC 564
 QY 187 HisArgArgAsnThrPheArgAlaSerLysIleMetGlnAlaArgAlaLeuGluAsnPro 206
 DB 565 CATAGGAGAGATGCTTTTAGAGCGCTTAAGATTATGCAGCAGCGAGCTTTGCTAATCCT 624
 QY 207 LysIleLysValLeuTrpAspSerGluValValGluAlaTyrGlyAlaAsnGlyGly 226
 DB 625 AAGATTGATGATTTGGAACTCGCTGTGTGGAGAGCTATGGAGATCGAGAAAGAGAT 684
 QY 227 ProLeuAlaGlyValLysValLysAsnLeuLeuAsnGlyGluValSerAspLeuGlnVal 246
 DB 685 GTCCTTGGAGGATTTGAAGTGAAGATGTTTACCGGAGATGTTTCTGATTTAAAGTT 744
 QY 247 SerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLysPheLeuGlyGlnLeu 266
 DB 745 TCTGGATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 804
 QY 267 GluLeuAspSerAspGlyTyrValGluThrLysProGlySerThrHisThrSerValLys 286
 DB 805 GAGTTAGATTCGATGTTATGTTGTCACGAGAGCTGGTACTACACAGACTAGCGTTCC 864
 QY 287 GlyValPheAlaAlaGlyAspValGlnAspLysLysTyrArgGlnAlaIleThrAlaAa 306
 DB 865 CGAGTTTTCCTGCGGCTGATGTTTCAGGATAAGAGTATAGGCAAGCCATCCTGCTGCA 924
 QY 307 GlySerGlyCysMetAlaAlaLeuAspAlaGluHisTyrLeuGlnGluIleGlyAlaGln 326
 DB 925 GGAACTGGGTGATGGCAGCTTTGGATGCGAGCATTACTTACAGAGATTGGATCTCAG 984
 QY 327 GluGlyLysSerAsp 331
 DB 985 CAAGGTAAGAGTGAT 999
 RESULT 10
 ABN89576
 ID ABN89576 standard; DNA; 1002 BP.
 XX AC ABN89576;
 XX 06-SEP-2002 (first entry)
 XX Arabidopsis NADPH thioredoxin reductase DNA SEQ ID NO:8.
 XX Multimeric protein; redox protein; thioredoxin; thioredoxin reductase;
 KW oil body; ophthalmological; antidiabetic; cytosolic; antiproliferative;
 KW vasotropic; vulnery; antibacterial; immunosuppressive; antitumor;
 KW food product; milk; wheat; oxidative stress; cataract; diabetes;
 KW chronic obstructive pulmonary disease; emphysema; psoriasis; sepsis;
 KW bronchiopulmonary disease; malignancy; reperfusion injury; wound healing;
 KW gastro intestinal bleeding; intestinal bowel disease; ulcer;
 KW gastro oesophageal reflux disease; gene; ds.
 XX Arabidopsis sp.
 OS

30-AUG-1999; 99US-0151303P. Length: 1375
Pred. No.: 135-128
Score: 135-50
Percent Similarity: 86.65%
Best Local Similarity: 76.56%
Query Match: 9
DB: 3

31-AUG-1999; 99US-0151438P.
31-AUG-1999; 99US-0151930P.
01-SEP-1999; 99US-0152363P.
07-SEP-1999; 99US-0153070P.
10-SEP-1999; 99US-0153758P.
13-SEP-1999; 99US-0154018P.
15-SEP-1999; 99US-0154039P.
16-SEP-1999; 99US-0154779P.
20-SEP-1999; 99US-0155139P.
22-SEP-1999; 99US-0155486P.
23-SEP-1999; 99US-0155659P.
24-SEP-1999; 99US-0156458P.
28-SEP-1999; 99US-0156596P.
29-SEP-1999; 99US-0157117P.
04-OCT-1999; 99US-0157753P.
05-OCT-1999; 99US-0157865P.
06-OCT-1999; 99US-0158023P.
07-OCT-1999; 99US-0158232P.
08-OCT-1999; 99US-0158369P.
12-OCT-1999; 99US-0159293P.
13-OCT-1999; 99US-0159294P.
13-OCT-1999; 99US-0159295P.
13-OCT-1999; 99US-0159329P.
14-OCT-1999; 99US-0159330P.
14-OCT-1999; 99US-0159331P.
14-OCT-1999; 99US-0159637P.
14-OCT-1999; 99US-0159638P.
18-OCT-1999; 99US-0159584P.
21-OCT-1999; 99US-0160741P.
21-OCT-1999; 99US-0160767P.
21-OCT-1999; 99US-0160768P.
21-OCT-1999; 99US-0160770P.
21-OCT-1999; 99US-0160814P.
21-OCT-1999; 99US-0160815P.
22-OCT-1999; 99US-0160980P.
22-OCT-1999; 99US-0160981P.
22-OCT-1999; 99US-0160989P.
22-OCT-1999; 99US-0161404P.
25-OCT-1999; 99US-0161405P.
25-OCT-1999; 99US-0161406P.
26-OCT-1999; 99US-0161359P.
26-OCT-1999; 99US-0161360P.
26-OCT-1999; 99US-0161361P.
26-OCT-1999; 99US-0161920P.
28-OCT-1999; 99US-0161932P.
28-OCT-1999; 99US-0161993P.
29-OCT-1999; 99US-0162142P.

Alignment Scores:
Pred. No.: 135-128
Score: 135-50
Percent Similarity: 86.65%
Best Local Similarity: 76.56%
Query Match: 9
DB: 3

US-10-005-429-25 (1-331) x AAC40213 (1-1375)

Qy 4 SerAlaAlaProLeu-----ArgThrArgIleCysIleIleGlySer 18
Db 128 TCOCGCCCGCCCGCCGCATCGACATGGAAACTCACAAAACCAGGTTCGCATCGTCCGAAGT 187

Qy 19 GlyProAlaAlaHisThrAlaAlaIleTyraAlaAargAlaGluleuLysProValLeu 38
Db 188 GMAACCAAGCAGCACAACGGGGGCGATCTATGATCGAGAGGGAGGCTTAAGCCTCTTCTC 247

Qy 39 PheGluGlyTrpMetAlaAsnAspIleAlaAlaGlyGlnLeuThrThrThrThrAsp 58
Db 248 TTCGAAGCATGGATGGCTAACGACATCGCTCCCGGGGGTCAATTAACTACACAACCGAC 307

Qy 59 ValGluAsnPheProGlyPheProAsnGlyIleMetGlyAlaAspLeuMetAspAncCys 78
Db 59 ValGluAsnPheProGlyPheProAsnGlyIleMetGlyAlaAspLeuMetAspAncCys 78

308 GTCGAAAACTCCCTGGGTTCCCTGAAGATNTCTCGGTATTGTATATCGTTTGAGAAATTC 367
79 ArgAlaGlnSerLeuArgPheGlyThrAsnIleLeuSerGluThrValThrAlaValAsp 98
368 AGAARACAAATCGGAGAGATTTCGAACATACGATCTTCACGGAAACTGTTTAAACAAAGTTGAT 427
99 PheSerAlaCysPropheArgValSerAlaAspSerThrThrValLeuAlaAspAlaVal 118
428 TTCTCATCGAAACCGTTTAAGCTATTCACTGATTTCGAGAATCTGTCTCGCTGATTTCTGTA 487
119 IleValAlaThrGlyValAlaValaAargLeuHisPheProGlySer----- 134
488 ATCACTTCTACCTGGAGCTGTGTAAACGCTCTTAGCTCACTGCTGCTGGTGAAGATAAT 547
135 AspAlaTyrrTpAsnArgGlyIleSerAlaCysAlaAlaValCysAspGlyAlaAlaProIle 154
548 CGTGGTTTTTGAACGCTGATCTCCGCTTGTGCTGTTTCGACGGAGCTGCTCCGAT 607
155 PheArgAsnLysProIleAlaValIleGlyGlyAspSerAlaMetGluGluSerAsn 174
608 TTTAGAAATAGCCCTCTTGTGGTTANTGTGGTGGTGATTTCAGCTATGAGAGAAAGCAAT 667
175 PheLeuThrLysTyrrGlySerHisValTyrrIlelleHisArgAsnThrPheArgAla 194
668 TTTCTGACTAAGTATCGATCTAAGGTTTTATATTATTCATAGAGGGATACCTTTAGGGCG 727
195 SerIlylleMetGlnAlaAargAlaLeuGluAsnProLysIleLysValLeuTriAspSer 214
728 TCTAAGATTATCGACAGAGACTTTGTCTAACCTTAGATTGAAGTGAATTTGGAATCT 787
215 GluValValGluAlaTyrrGlyGlyAlaAsnGlyGlyProLeuAlaGlyValLysVallys 234
788 GCCGTGTTGAGGCGTATGGTGATGAAAATGGACGCTGTTCTTGGAGGATTCGAAGTGAAG 847
235 AsnLeuLeuAsnGlyGluValSerAspLeuGlnValSerGlyLeuPhePheAlaIleGly 254
848 AATGTTGTTACTGGGGATGTTTCAGATCTGAAGGTCTCTGGATTGTTCTTTGCTATTGGT 907
255 HisGluProAlaThrLysPheLeuGlyGlyGlnLeuGluLeuAspSerAspGlyTyrrVal 274
908 CATGACCCAGCTACGAGTTTTCGATGGCAGCTTGAGCTTGATGAAGATGTTATGTT 967
275 GluThrLysProGlySerThrHisThrServalysGlyValPheAlaAlaGlyAspVal 294
968 GTGACCAACCCAGGTACTACTAAGACGAGCGGTGGTGGTATTGCTGCTGGAGATGTT 102
295 GlnAspLysLysTyrrArgGlnAlaIleThrAlaAlaGlySerGlyCysMetAlaAlaLeu 314
1028 CAACACAAAGATATAGACAGCCATCACTGCTGAGGACCTGGTGGTGGTGGCGCATTTG 1087
315 AspAlaGluHisTyrrLeuGlnGluIleGlyAlaGlnGluGlyLysSerAsp 331
1088 GATGACAGACATTACTTACAGAGATGGATCTCAGGAGGGTAAGAGTGAAT 1138

RESULT 9
ABN89578 ID ABN89578 standard; DNA, 1002 BP.
XX AC ABN89578;
XX DT 06-SEP-2002 (first entry)
XX DE Arabidopsis NADPH thioredoxin reductase DNA SEQ ID NO:10.
XX Multimeric protein; redox protein; thioredoxin; thioredoxin reductase;
XX oil body; ophthalmological; antidiabetic; cytosolic; antiparasitic;
XX vasotropic; vulnary; antibacterial; immunosuppressive; antiulcer;
XX food product; milk; wheat; oxidative stress; cataract; diabetes;
XX chronic obstructive pulmonary disease; envenomation; psoriasis; sepsis;
XX bronchiopulmonary disease; malignancy; reperfusion injury; wound healing;
XX gastro intestinal bleeding; intestinal bowel disease; ulcer;
XX gastro oesophageal reflux disease; gene; ds.

DE Arabidopsis thaliana DNA fragment SEQ ID NO: 56668.
XX Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
XX EP1033405-A2.
XX
XX 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-00301439.
XX
PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 23-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 06-MAY-1999; 99US-0132487P.
PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 04-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 05-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 06-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.

QY 195 SerLysIleMetGlnAlaArgAlaLeuGluAenProLysValLeuThrPaspSer 214
DB 739 TCTAAGATTATGAGCAGAGAGCTTGTCTTAACCCCTAAGATTGAAGTATTGGAATCT 798
QY 215 GluValValGluAlaValGlyGlyAlaAenGlyGlyProLeuAlaGlyValLys 234
DB 799 GCCGTGTTGAGCGGATGATGATAAATGACGCTTCTTGGAGGATTGAAGGTGAAG 858
QY 235 AsnLeuLeuAenGlyGlyValSerAspLeuGlnValSerGlyLeuPheAlaIleGly 254
DB 859 AATGTTGTTACTGGGATGTTTCTAGATCTGAAGGTCTCTGATGTTCTTGTATGTT 918
QY 255 HisGluProAlaThrLysPheLeuGlyGlyGlnLeuGluLeuAspSerAspGlyVal 274
DB 919 CATGACCGAGCTACGAGTTTGTGATGGCAGCTTGTGAGCTTGATGAAGTATGTT 978
QY 275 GluThrLysProGlySerThrHisThrSerValLysGlyValPheAlaGlyAspVal 294
DB 979 GTGACCAAGCCAGGTACTTAAGACGAGCGGTGTTGTTGTTGTTGTTGTTGTTGTT 1038
QY 295 GlnAspLysValSerArgGlnAlaIleThrAlaAlaGlySerGlyCysMetAlaAlaLeu 314
DB 1039 CAAGCAAGAGATATAGACAGGCTATCTGCTGACGAGTCTGGTGGTGGTGGTGGT 1098
QY 315 AspAlaGluHisThrLeuGlnGluIleGlyAlaGlnGluGlyLysSerAsp 331
DB 1099 GATGACAGGATTTACTTACAGAGATTGGATCTCAGAGCGGTAAAGATGAT 1149

RESULT 6
ABZ14681
ID ABZ14681 standard; DNA; 1152 BP.

XX ABZ14681;
XX
XX
XX 21-JAN-2003 (first entry)
XX Arabidopsis thaliana stress regulated gene SEQ ID NO 2486.
XX Arabidopsis thaliana; plant; gene; stress; transgenic; ds.
XX Arabidopsis thaliana.
XX
XX WO200216655-A2.
XX
XX 28-FEB-2002.
XX
XX 24-AUG-2001; 2001WO-US026685.
XX
XX 24-AUG-2000; 2000US-0227866P.
XX 26-JAN-2001; 2001US-0264647P.
XX 22-JUN-2001; 2001US-0300111P.

XX (SCRI) SCRIPPS RES INST.
XX (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
XX Harper JF, Kreps J, Wang X, Zhu T;
XX WPI; 2002-304127/34.
XX
XX Identifying a stress condition to which a plant cell has been exposed and
XX producing plants with increased tolerance to these abiotic stresses.
XX
XX Claim 144; SEQ ID NO 2486; 577pp + Sequence Listing; English.

XX The invention relates to identifying a stress condition to which a plant
XX cell has been exposed, comprising: (a) contacting nucleic acid
XX representative of expressed polynucleotides in the plant cell with an
XX array or probes representative of the plant cell genome; and (b)
XX detecting a profile of expressed polynucleotides in the plant cell
XX characteristic of a stress response. The method is useful in the
XX production of transgenic plants, cells and seeds and in producing plants
XX with increased tolerance to abiotic stress. The present sequence is that
XX of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used

CC in methods of the invention. Note: The sequence data for this patent is
CC not represented in the printed specification but is based on sequence
CC information supplied to Derwent by the European Patent Office
XX
SQ Sequence 1152 BP; 281 A; 222 C; 308 G; 341 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 1.18e-128 Length: 1152
Score: 1335.50 Matches: 258
Percent Similarity: 86.65% Conservative: 34
Best Local Similarity: 76.56% Mismatches: 36
Query Match: 78.15% Indels: 9
DB: 6 Gaps: 2
US-10-005-429-25 (1-331) x ABZ14681 (1-1152)

QY 4 SerAlaAlaAlaProLeu-----ArgThrArgIleCysIleIleGlySer 18
DB 139 TCCGCGCGCGCGCGCGTGCACATGGAAGAACTCAAAACACAGGTTTGCATGTCGAAGT 198
QY 19 GlyProAlaAlaHisThrAlaAlaIleTyrAlaAlaArgAlaGluLeuLysProValLeu 38
DB 199 GGACCCAGCAGCACACACGCGCGGATCTATGCATCGAGAGCGGAGCTTAAGCCTCTCTC 258
QY 39 PheGluGlyTrpMetAlaAsnAspIleAlaAlaGlyGlyGlnLeuThrThrThrAsp 58
DB 259 TTCGAGGATGGATGCTTAACGACATCGCTCCCGCGGTCAATTAACTACACAAACCCGAC 318
QY 59 ValGluAenPheProGlyPheProAsnGlyIleMetGlyAlaAspLeuMetAspAsnCys 78
DB 319 GTCGAATCTTCCCTGGGTCCCTGAGGATATTCGGTATTGATATCGTTGAGAAATTC 378
QY 79 ArgAlaGlnSerLeuArgPheGlyThrAsnIleLeuSerGluThrValThrAlaValAsp 98
DB 379 AGAAAAACAATCGAGAGATTTGGAATCTACGATCTTCAACGAAACTGTTAAACAAAGTTGAT 438
QY 99 PheSerAlaCysProPheArgValSerAlaAspSerThrValLeuAlaAspAlaVal 118
DB 439 TTCTCATCGAACCCTTTAAGCTATCTAGTATCGAGACTGTTCTGCTGATCTGTAT 498
QY 119 IleValAlaThrGlyAlaValAlaArgArgLeuHisPheProGlySer----- 134
DB 499 ATCAATTTCTACTGGAGCTGTTGCTAAACGCTTACGCTTCACTGGATCTGTTGAAGGTAAT 558
QY 135 AspAlaTyrrTrpAsnArgGlyIleSerAlaCysAlaValCysAspGlyAlaAlaProIle 154
DB 559 GGTGTTTGTGAATCGTGTATCTCCGCTTGTGCTGTTGCTGCTGCTGCTGCTGCTGCT 618
QY 155 PheArgAsnLysProIleAlaValIleGlyGlyGlyAspSerAlaMetGluGluSerAsn 174
DB 619 TTTAGGATTAACCTCTTGTGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 678
QY 175 PheLeuThrLysTyrrGlySerHisValTyrIleIleHisArgArgAsnThrPheAlaGla 194
DB 679 TTTCTGACTAAGTATGGATCTAAGGTTTATATATATTCATAGAGGATACGTTTAGGGCG 738
QY 195 SerLysIleMetGlnAlaArgAlaLeuGluAenProLysValLeuThrPaspSer 214
DB 739 TCTAAGATTATGAGCAGAGAGCTTGTCTTAACCCCTAAGATTGAAGTATTGGAATCT 798
QY 215 GluValValGluAlaValGlyGlyAlaAenGlyGlyProLeuAlaGlyValLys 234
DB 799 GCCGTGTTGAGCGGATGATGATAAATGACGCTTCTTGGAGGATTGAAGGTGAAG 858
QY 235 AsnLeuLeuAenGlyGlyValSerAspLeuGlnValSerGlyLeuPheAlaIleGly 254
DB 859 AATGTTGTTACTGGGATGTTTCTAGATCTGAAGGTCTCTGATGTTCTTGTATGTT 918
QY 255 HisGluProAlaThrLysPheLeuGlyGlyGlnLeuGluLeuAspSerAspGlyVal 274
DB 919 CATGACCGAGCTACGAGTTTGTGATGGCAGCTTGTGAGCTTGATGAAGTATGTT 978
QY 275 GluThrLysProGlySerThrHisThrSerValLysGlyValPheAlaGlyAspVal 294

```
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144864P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145132P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149386P.
PR 17-AUG-1999; 99US-0149417P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158312P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.

PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161922P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Alignment Scores:
Pred. No.: 1,18e-128
Score: 1335.50
Percent Similarity: 86.65%
Best Local Similarity: 78.56%
Query Match: 76.15%
DB: 3

US-10-005-429-25 (1-331) x AAC43307 (1-1152)

QY 4 SerAlaAlaProLeu-----ArgThrArgileCysIleIleGlySer 18
DB 139 TCCGCCGCCGCCGCCGCCGACATGCAACCAACCAAGTTTCATCGTCGGAAT 198
QY 19 GlyProAlaAlaHisThrAlaAlaIleTyrAlaAlaArgAlaGluLeuLysProValLeu 38
DB 199 GGACCAGCAGCACACACGGCGGGGATCTATGATCGATGAGCGGAGCTTAAGCCTCTCTC 258
QY 39 PheGluGlyTrpMetAlaAsnAspIleAlaAlaGlyGlyGlnLeuThrThrThrAsp 58
DB 259 TTCGAGGATGGATGGCTTAACGATCGCTCCCGGGGTCAATTAACCTACCAACCGAC 318
QY 59 ValGluAsnPheProGlyPheProAsnGlyIleMetGlyAlaAspLeuMetAspAsnCys 78
DB 319 GTCGAAACCTCCCTGGGTTCCCTGAAGGTATTCGGTATTGATATCGTTGAGAAATTC 378
QY 79 ArgAlaGlnSerLeuArgPheGlyThrAsnIleLeuSerGluThrValThrAlaValAsp 98
DB 379 AGAAACCAATCGGAGAGATTTGGAATCAAGTCTTCACGGAACCTGTTAACAAAGTTGAT 438
QY 99 PheSerAlaCysPropheArgValSerAlaAspSerThrThrValLeuAlaAspAlaVal 118
DB 439 TTCTCATCGAAACCGTTTAAGTATTCACTGATTTCGGAACCTGTTCTGCTGATCTGTA 498
QY 119 IleValAlaThrGlyAlaValAlaArgArgLeuHisPheProGlySer----- 134
DB 499 ATCAATTTCTAGGAGCTGTTGTGAACGCTTAGCTTAGCTTCACTGATCTGGTGAAGTAAT 558
QY 135 AspAlaTyrTrpAsnArgGlyIleSerAlaCysAlaValCysAspGlyAlaAlaProIle 154
DB 559 GGTGGTTTTTGAATCGTGATACTCCGCTTGTGCTTGTGCTTGGCAGCGAGCTGCTCGAAT 618
QY 155 PheArgAsnLysProIleAlaValIleGlyGlyAspSerAlaMetGluGluSerAsn 174
DB 619 TTTAGGAATAGCCCTCTGTGGTATTGGTGGTGGTATTCAGCTATGAGGAAGCGAAT 678
QY 175 PheLeuThrLysTyrGlySerHisValTyrIleIleHisArgArgAsnThrPheArgAla 194
DB 679 TTCTGACTAAGTATGATCTAAGGTTTATATTATTATTATTATTATTATTATTATTATTAGGGG 738
```

Db 361 GCACCGCGCGCTGCGCGCGGAGCTCCACTTTCGCGGCTCCGACGCTTACTGGAACGCG 420
QY 141 GlyIleSerAlaCysAlaValCysAspGlyAlaAlaProIlePheArgAsnLysProIle 160
Db 421 GGCATCTCGCGCTGCGCGCGGCTGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480
QY 161 AlaValIleGlyGlyGlyAspSerAlaMetGluSerAsnPheLeuThrLysTyrGly 180
Db 481 GCGTCATCG 540
QY 181 SerHisValTyrIleIleHisArgArgAsnThrPheArgAlaSerLysIleMetGlnAla 200
Db 541 TCCCATGTGTACATCATCCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 500
QY 201 ArgAlaLeuGluAsnProLysIleLysValLeuPhePheAlaIleGlyHisGluProAlaThrLys 220
Db 601 AGGCGCTTGTCAACCCAGATCCAGTTTCTGGGACTCTGAGGTCTGAGGCTGAGGCTAC 560
QY 221 GlyGlyAlaAsnGlyGlyProLeuAlaGlyValLysValLysValLysValLysValLys 240
Db 661 GCG 699
QY 241 ValSerAspLeuGlnValSerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLys 260
Db 700 -----GGTTCGGTCTCTTCTTCCCATCGACATGACCGCGCGCGCGCGCGCG 744
QY 261 PheLeuGlyGlyGlnLeuGluLeuAspSerAspGlyTyrValGluThrLysProGlySer 280
Db 745 TTCTCTCG 804
QY 281 ThrHisThrSerValLysGlyValPheAlaAlaGlyAspValGlnAspLysLysTyrArg 300
Db 805 ACCACACACCATGTGAAGGGGGTCTTGTGCTGGGGATGTGAGGACAAAGATATCGC 864
QY 301 GlnAlaIleThrAlaAlaGlySer-----GlyCys 310
Db 865 CAGGCTATTACTCGCGCTGGATCAGACATCAGTTCGTTGATGGTTGC 912
RESULT 5
AAC43307
ID AAC43307 standard; DNA; 1152 BP.
XX
AC AAC43307;
XX
XX 17-OCT-2000 (first entry)
XX
XX Arabidopsis thaliana DNA fragment SEQ ID NO: 38790.
XX
XX Hybridisation assay; genetic mapping; gene expression control;
XX protein identification; signal transduction pathway; metabolic pathway;
XX promoter; termination sequence; ss.
XX Arabidopsis thaliana.
XX
XX EP1033405-A2.
XX
XX 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-00301439.
XX
XX 25-FEB-1999; 99US-0121825P.
XX 05-MAR-1999; 99US-0123180P.
XX 09-MAR-1999; 99US-01231548P.
XX 23-MAR-1999; 99US-0125788P.
XX 23-MAR-1999; 99US-0126264P.
XX 29-MAR-1999; 99US-0126785P.
XX 01-APR-1999; 99US-0127462P.
XX 06-APR-1999; 99US-0128234P.
XX 08-APR-1999; 99US-0128714P.
XX 16-APR-1999; 99US-0129845P.
XX 19-APR-1999; 99US-0130077P.
XX 21-APR-1999; 99US-0130449P.

PR 23-APR-1999; 99US-0130510P.
PR 23-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 06-MAY-1999; 99US-0132487P.
PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.

CC reductase eliminates the need to develop exogenous sources for addition
CC during processing. Secondly, physical disruption of seed integrity is not
CC necessary to bring the enzyme in contact with the storage or matrix
CC proteins of the seed prior to processing or as an extra processing step.
CC The present sequence is rice NADPH dependent thioredoxin reductase DNA
CC (NTR)

Sequence 1560 BP: 302 A; 435 C; 439 G; 372 T; 0 U; 12 Other;

Alignment Scores:	
Pred. No.:	2,97e-143
Score:	1478.00
Length:	1560
Percent Similarity:	96.12%
Matches:	282
Best Local Similarity:	91.56%
Conservative:	15
Mismatches:	12
Query Match:	86.48%
Indels:	0
DB:	5
Gaps:	0

US-10-005-429-25 (1-331) X AAD29838 (1-1560)

Qy	1	MetGluGlySerAlaAlaAlaProLeuArgThrArgIleCysIleIleGlySerGlyPro	20
Db	406	ATCGAGGGATCGCGCGGGGGCGCGCTCCGACGCGCTGTGCATCATTCGGAGGGGGCGG	465
Qy	21	AlaAlaHisThrAlaAlaIleTyrAlaAlaArgAlaGluLeuIysProValLeuPheGlu	40
Db	466	TCGGCGRCACGGCGCGGATCTACGCGCGCGCGGAGTCTAAGCCGCTGTCTTCGAG	525
Qy	41	GlyTrpMetAlaAsnAspIleAlaAlaGlyGlyGlnLeuThrThrThrThrAspValGlu	60
Db	526	GGCTGGCTGCCAACGACATCGCGCGCGGGGGCGAGTCTACCAACCACACCGAGCTCGAG	585
Qy	61	AsnPheProGlyPheProAsnGlyIleMetClyAlaAspLeuMetAspAsnCysArgAla	80
Db	586	AACCTCCCGGGGTCCCGAGGGGATCTCTCGCGCGGAGTCTATGATTCGGTCCGCGGCC	645
Qy	81	GlnSerLeuArgPheGlyThrAsnIleLeuSerGluThrValThrAlaValAspPheSer	100
Db	646	CAGTCCCTCCGTTTCGGCACGACATCATCTCCGAGACCGTCAACGCGGTTCGACTTCCTC	705
Qy	101	AlaCysProPheArgValSerAlaAsnSerThrThrValLeuAlaAspAlaValIleVal	120
Db	706	GCCGCGCCCTTCGCGTGCCTCCGATCTCACACCGTGTCTGCGCGAGCGGTGCTGCTC	765
Qy	121	AlaThrGlyAlaValAlaArgArgLeuHisPheProGlySerAspAlaTyrTrpAsnArg	140
Db	766	GCCACCGCGCGCTTCGCGCGGACTCCACTTCGCGCGCTCCGACGCGCTACTTGAACCGC	825
Qy	141	GlyIleSerAlaCysAlaValCysAsnGlyAlaAlaProIlePheArgAsnLysProIle	160
Db	826	GGCATCTCAGCTCGCGCGTCTCGGACGGGGCGGCCCAATCTTCAGAAACAACCCATC	885
Qy	161	AlaValIleGlyGlyIysAspSerAlaMetGluGluSerAsnPheLeuThrLysTyrGly	180
Db	886	GCGTCTATCGCGCGCGGAGCTCCGCCATCGAGGAGTCCAACTTCCTCACCAAGTACGGC	945
Qy	181	SerHisValTyrIleIleHisArgArgAsnThrPheArgAlaSerLysIleMetGlnAla	200
Db	946	TCCCATGTGTACATCATCCACGCGCGCAACACCTTCGCGCGCTCCAGATCATCAGCGCC	1005
Qy	201	ArgAlaLeuGluAsnProLysIleLysValLeuTrpAspSerGluValValGluAlaTyr	220
Db	1006	AGGCGGTGTCAACCCCAAGATCCAGGTTTCTGGGACTCTGAGGTCTGTTCGAGCGCTAC	1065
Qy	221	GlyGlyAlaAsnGlyGlyProLeuAlaGlyValIysValIysAsnLeuLeuAsnGlyGlu	240
Db	1066	GGCGCGGAGGTGAGGTCCATTGGCTGTGTCAAGGTGAGAACTTGGTTACTTGGGAAG	1125
Qy	241	ValSerAspLeuGlnValSerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLys	260
Db	1126	ATCTCCGACCTTCAGGTGTCCGGTCTCTTCTTCGCCATCGGACATGAACCGCGGACGAAG	1185
Qy	261	PheLeuGlyGlyGlnLeuGluLeuAspSerAspGlyTyrValGluThrLysProGlySer	280

Db	1186	TTTCTCGCGCGGACGCTTGGAGCTCGATGCGGTATGTGGCCACCAAGCCAGGCTCC	1245
Qy	281	ThrHisThrSerValLysGlyValPheAlaAlaGlyAspValGlnAspLysLysTyrArg	300
Db	1246	ACGCACACCAAGTGTGAAGGGGGCTTTGCTGCTGGGGATGTGCAGGCAAGAAGATATGCG	1305
Qy	301	GlnAlaIleThrAlaAlaGlySerGly	309
Db	1306	CAGGCTATTACTGCGCGCTGGATCAGGT	1332

RESULT 3
ADA70761
IN ADA70761 standard: DNA: 1130 BP.

AC ADA70761;

20-NOV-2003 (first entry)

XX Rice gene. SEQ ID 4084.

XX plant; bacterial infection; fungal infection; viral infection; rice
KW gene; ds.

OS Orvza sativa.

IX
DN
W0200300898-21

XX 00-777-2003

XX 5

XX

XX
XX

XX

PI
Chang H, Cooper S, Graedtke S, Goll SA, Zou Z, Zou G;
Katagiri E, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;

XX
DP
WPT: 2003-175290/17

XX Identifying at least one gene involved in plant resistance or response to
PT pathogenic infection for conferring resistance or tolerance to a plant to
PT bacterial, fungal or viral infection by determining or detecting plant
PT gene expression.

PS Claim 6: SEQ ID NO 4084: 899bp: English.

The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1 comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to illustrate the invention.

Sequence 1130 BP: 174 A: 419 C: 358 G: 179 T: 0 U: 0 Other:

Alignment Scores:		
Score No.:	2.75e-136	Length:
Pred.	1409.00	Matches:
Percent Similarity:	94.81%	Mismatches:
Best Local Similarity:	87.34%	Gaps:
Query Match:	82.45%	Indels:
DB:	7	0
	0	0
		1130

US-10-005-429-25 (1-331) x ADA70761 (1-1130)

1 MotC1::C1vSerA] a d i a d] a B r o I e u B r t t h r A r t l e C v s r l e t l e G l y s e r G l y p r o 20

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1

DR P-PSDB; AAB29250.
XX Recombinant or isolated nucleic acid, useful for producing transgenic
PT plants with altered redox properties, encode thioredoxin h or thioredoxin
PT reductase.

XX Claim 66; Fig 5B; 125pp; English.

XX The present invention relates to the isolation and use of the barley
CC thioredoxin h and NADPH-thioredoxin reductase coding and protein
CC sequences. Thioredoxin is thought to be involved in plant development via
CC its function in the reduction of disulfide bridges. Thioredoxin can be
CC used in hair care products and in the neutralisation of some venoms and
CC toxins, and is also useful in the reduction of some food, for example it
CC can be used to reduce the allergenicity of foods and the digestibility of
CC some proteins. It can also be used to enhance the baking qualities of
CC cereal flour

XX Sequence 1991 BP; 338 A; 675 C; 591 G; 368 T; 0 U; 19 Other;

Alignment Scores:

Pred. No.: 9.54e-150 Length: 1991
Score: 1542.00 Matches: 302
Percent Similarity: 94.26% Conservative: 10
Best Local Similarity: 91.24% Mismatches: 19
Query Match: 90.23% Indels: 1
DB: 3 Gaps: 0

US-10-005-429-25 (1-331) x AAC62460 (1-1991)

Qy 1 MetGluGlySerAlaAlaAlaProLeuArgThrArgIleCysIleGlySerGlyPro 20
Db 1 ATGGAGGATTCG 60
Qy 21 AlaAlaHisThrAlaAlaIleTyAlaAlaArgAlaGluLeuLysProValLeuPheGlu 40
Db 61 GCCGCGCACACG 120
Qy 41 GlyTrpMetAlaAsnAspIleAlaAlaGlyGlyGlnLeuThrThrThrAspValGlu 60
Db 121 GCCTCGATGCGCCACGACATCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
Qy 61 AsnPheProGlyPheProAsnGlyIleMetGlyAlaAspLeuMetAspAsnCysArgAla 80
Db 181 AACTTCCCGGATTCGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240
Qy 81 GlnSerLeuArgPheGlyThrAsnIleLeuSerGluThrValThrAlaValAspPheSer 100
Db 241 CAGTCCGTCGCGTTCGCGCACCAACATCCCTCCGAGACCGTCCCGAGGTTCGCTTCC 300
Qy 101 AlaCysProPheArgValSerAlaAspSerThrThrValLeuAlaAspAlaValIleVal 120
Db 301 GCCCGCCCTTCGGGTCACCTCCGACTCCGACCGCTCTCCGCGACANCGTCGCTC 360
Qy 121 AlaThrGlyAlaValAlaArgArgLeuHisPheProGlySerAspAlaTyTrpAsnArg 140
Db 361 GCCCG 419
Qy 141 GlyIleSerAlaCysAlaValCysAspGlyAlaAlaProIlePheArgAsnLysProIle 160
Db 420 GGCATCTCCGCTCGCGCTGCGAGCGCGCTGCGAGCGCGCGCGCGCGCGCGCGCGCG 479
Qy 161 AlaValIleGlyGlyAspSerAlaMetGluGluSerAsnPheLeuThrLysTyGly 180
Db 480 GCGGTTCATCG 539
Qy 181 SerHisValTyIleIleHisArgArgAsnThrPheArgAlaSerLysIleMetGlnAla 200
Db 540 TCCCAAGTGTATCATCATCATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 599
Qy 201 ArgAlaLeuGluAsnProLysIleValLeuTrpAspSerGluValValGluAlaTy 220
Db 600 AGGCGCGCTTCCAAATCCTAAGATCCNGGTTGTCTGGGACTCGGAGTCTCGAGGCTTAC 659

Qy 221 GlyGlyAlaAsnGlyGlyProLeuAlaGlyValLysValLysAsnLeuLeuAsnGlyGlu 240
Db 660 GCGCGTGCAGCG 719
Qy 241 ValSerAspLeuGlnValSerGlyLeuPheAlaIleGlyHisGluProAlaThrLys 260
Db 720 GTGTCTACCTTCAGGTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 779
Qy 261 PheLeuGlyGlyGlnLeuGluLeuAspSerAspGlyTyValGluThrLysProGlySer 280
Db 780 TTCTCAATCG 839
Qy 281 ThrHisThrSerValLysGlyValPheAlaAlaGlyAspValGlnAspLysLysTyArg 300
Db 840 ACACATACCAAGTGGAGGCGGCTTTTCCTGCTGCGACGTCACAGGATAGAAGTATCG 899
Qy 301 GlnAlaIleThrAlaAlaGlySerGlyCysMetAlaAlaLeuAspAlaGluHisTyLeu 320
Db 900 CAGGCCATTACTGCTGCTGCGATCAGGTTGCGATGCTGCTTGGACGCGCGACTACTG 959

RESULT 2

AAD29838
ID AAD29838 standard; DNA; 1560 BP.

XX
AC AAD29838;

DT 17-MAY-2002 (first entry)

DE Rice NADPH dependent thioredoxin reductase DNA (NTR).

XX Transgenic plant; thioredoxin reductase; starch; protein; grain;
KW milling process; enzyme; rice; ds.

OS Oryza sativa.

XX FH Key Location/Qualifiers
FT CDS 406..1338
FT /*tag= a
FT /product= "Rice NTR"

XX PN WO200198509-A2.
XX PD 27-DEC-2001.

XX PF 19-JUN-2001; 2001WO-EP006918.
XX PR 21-JUN-2000; 2000US-00598747.

XX PA (SYGN) SYNGENTA PARTICIPATIONS AG.
XX PI Lanahan MB, Desai NM, Gasdaaka PY;

XX DR WPI; 2002-179557/23.
XX P-PSDB; AAE18733.

XX Transgenic plant coding for eukaryotic thioredoxin reductase at elevated
PT levels useful for separating the starch and protein components of grain
PT in a milling process.

XX PS Claim 12; Page 81; 86pp; English.

XX The present invention relates to a transgenic plant comprising
CC heterologous DNA coding for eukaryotic thioredoxin reductase integrated
CC into its nuclear or plastid genome and use of thioredoxin reductase for
CC separating the starch and protein components of grain in a milling
CC process. Transgenic plant is used for separating the starch and protein
CC components of grain in a milling process. Transgenic plant may be used to
CC produce thioredoxin reductase at elevated levels. Delivery of thioredoxin

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 5, 2004, 00:59:23 ; Search time 425.882 Seconds
(without alignments)
3301.746 Million cell updates/sec

Title: US-10-005-429-25

Perfect score: 1709

Sequence: 1 MEGSAAPLRICIGSGP.....AALDAHYLQIQAQEGKSD 331

Scoring table: BLOSUM62

Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DBV=xlp
-Q=/cgn2.1/USPTO.spool_p/US10005429/runat_04052004_121648_15427/app.query.fasta_1.782
-DB=N Geneseq 29Jan04 -QFMT=fastap -SUPPLX=p2n.rng -MINMATCH=0.1 -LOOPEL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -LOCALIGN=200 -THR SCORE=0.5 -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10005429 -CGN_1_1_886 -runat_04052004_121648_15427 -NCFU=6 -ICFU=3
-NO MWAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N Geneseq 29Jan04: *
1: Geneseqn1980s: *
2: Geneseqn1990s: *
3: Geneseqn2000s: *
4: Geneseqn2001as: *
5: Geneseqn2001bs: *
6: Geneseqn2002as: *
7: Geneseqn2003as: *
8: Geneseqn2003bs: *
9: Geneseqn2003cs: *
10: Geneseqn2004as: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1542	90.2	1991	3 AAC62460	Aac62460 Barley NA
2	1478	86.5	1560	6 AAD29838	Aad29838 Rice NADP
3	1409	82.4	1130	7 ADA70761	Ada70761 Rice gene
4	1365	79.9	963	7 ADA70332	Ada70332 Rice gene
5	1335.5	78.1	1152	3 AAC43307	Aac43307 Arabidops
6	1335.5	78.1	1152	6 ABZ14681	Abz14681 Arabidops
7	1335.5	78.1	1152	7 ADA67905	Ada67905 Arabidops
8	1335.5	78.1	1375	3 AAC48213	Aac48213 Arabidops

9	1318	77.1	1002	6 AEN89578	Abn89578 Arabidops
10	1318	77.1	1002	6 AEN89576	Abn89576 Arabidops
11	1318	77.1	1002	6 ABS53094	Abss53094 DNA encod
12	1318	77.1	1438	3 AAC38830	Aac38830 Arabidops
13	1318	77.1	1539	3 AAC36511	Aac36511 Arabidops
14	1318	77.1	3787	6 AEN89582	Abn89582 Phascolin
15	1318	77.1	3787	6 ABS53098	Abss53098 cDNA enco
16	1318	77.1	4545	6 AEN89584	Abn89584 Phascolin
17	1318	77.1	4545	6 ABS53100	Abss53100 DNA encod
18	1318	77.1	4546	6 AEN89583	Abn89583 Phascolin
19	1318	77.1	4546	6 ABS53099	Abss53099 DNA encod
20	1318	77.1	6357	7 AAL54488	Aal54488 Thioedox
21	1318	77.1	6357	7 AAL54492	Aal54492 Thioedox
22	1318	77.1	6357	9 ADD26530	Add26530 Thalecres
23	1318	77.1	6357	9 ADD26526	Add26526 Thalecres
24	1317	77.1	1540	3 AAC51123	Aacs1123 Arabidops
25	1306	76.4	6357	7 AAL54485	Aal54485 Thioedox
26	1306	76.4	6357	9 ADD26523	Add26523 Thalecres
27	1306	76.4	6357	9 ADD26533	Add26533 Thalecres
28	1305	76.4	6357	7 AAL54487	Aal54487 Thioedox
29	1305	76.4	6357	9 ADD26525	Add26525 Thalecres
30	1304	76.3	6357	7 AAL54494	Aal54494 Thioedox
31	1304	76.3	6357	7 AAL54484	Aal54484 Thioedox
32	1304	76.3	6357	9 ADD26528	Add26528 Thalecres
33	1304	76.3	6357	9 ADD26532	Add26532 Thalecres
34	1304	76.3	6357	9 ADD26532	Add26532 Thalecres
35	1304	76.3	6357	9 ADD26532	Add26532 Thalecres
36	1303	76.2	6357	7 AAL54493	Aal54493 Thioedox
37	1303	76.2	6357	9 ADD26531	Add26531 Thalecres
38	1303	76.2	6357	9 ADD26534	Add26534 Thalecres
39	1302	76.2	6357	9 ADD26524	Add26524 Thalecres
40	1302	76.2	6357	9 ADD26517	Add26517 Thalecres
41	1302	76.2	6408	7 AAL54482	Aal54482 Thioedox
42	1298	76.0	6306	7 AAL54479	Aal54479 Thioedox
43	1298	76.0	6356	9 ADD26529	Add26529 Thalecres
44	1298	76.0	6357	7 AAL54491	Aal54491 Thioedox
45	1298	76.0	6357	9 ADD26520	Add26520 Thalecres

ALIGNMENTS

RESULT 1

AAC62460

ID AAC62460 standard; DNA; 1991 BP.

XX AAC62460;

XX AC AAC62460;

XX DT 07-FEB-2001 (first entry)

XX DE Barley NADPH-thioedoxin reductase coding sequence.

XX KW Barley; NADPH-thioedoxin reductase; disulfide bridge reduction; NTR;

XX KW development; thioedoxin h; hair care product; venom neutralisation;

XX KW food technology; food allergy; ds.

XX OS Hordeum vulgare.

XX PN WO200058352-A2.

XX PD 05-OCT-2000.

XX PF 31-MAR-2000; 2000WO-US008566.

XX PR 31-MAR-1999; 99US-0127198P.

XX PR 06-DEC-1999; 99US-0169162P.

XX PR 21-JAN-2000; 2000US-017739P.

XX PR 21-JAN-2000; 2000US-0177740P.

XX PA (REGC) UNIV CALIFORNIA.

XX PI Cho M, Del Val G, Caillaud M, Lemaux PG, Suchanan BP;

XX WPI; 2000-679291/66.

XX DR

QY 79 ArgAlaGlnSerLeuArgPheGlyThrAsnIleLeuSerGluThrValThrAlaValAsp 98
 Db 65537 AGAAAACAATCGGAGAGATTGGAACTACGATCTTCAACGAACTGTTAACAAAGTTGAT 65596
 QY 99 PheSerAlaCysProPheArgValSerAlaAspSerThrThrValLeuAlaAspAlaVal 118
 Db 65597 TTCTCATCGAAACCGTTTAAGCTATTCTACTGATTGAGAACGTGTTCTGCTGATTTCTGTA 65656
 QY 119 IleValAlaThrGlyValAlaAlaArgArgLeuHisPheProGlySer----- 134
 Db 65657 ATCATTTCTACTGGAGCTGTGCTAAACGCTTTAGCTTCACTGGATCTGGTGAAGGTAAT 65716
 QY 135 AspAlaIleThrAsnArgGlyIleSerAlaCysAlaValCysAspGlyAlaAlaProIle 154
 Db 65717 GGTGGTTTTTGGAACTCGTGATATCCGCTTGTGCTGTTTTCGACGGAGCTGCTCCGATT 65776
 QY 155 PheArgAsnLysProIleAlaValIleGlyGlyGlyAspSerAlaMetGluGluSerAsn 174
 Db 65777 TTTAGGAATAAGCCTCTTGCTGTTATTTGGTGTGTTGATTCAGCTATGGAGGAGCGAAT 65836
 QY 175 PheLeuThrLysThrGlySerHisValTyrIleIleHisArgArgAsnThrPheArgAla 194
 Db 65837 TTTCTGACTAAGTATGCGATCTAAGGTTTATATATTATTCATAGGAGGATAOCTTTAGGGCG 65896
 QY 195 SerLysIleMetGlnAlaArgAlaLeuGluAsnProLysIleLysValIleuTrpAspSer 214
 Db 65897 TCTAAGATTATACAGCAGAGACTTTGCTTAACCTTAGATTGAGTGTGATTGGAACTCT 65956
 QY 215 GluValValGluAlaTyrGlyGlyAlaAsnGlyGlyProLeuAlaGlyValLysValLys 234
 Db 65957 GCCGTGGTTTGGCGGTATGGTGATGAAATGGACGTTCTTTGGAGGATTGAAGGTGAAG 66016
 QY 235 AsnLeuLeuAsnGlyGluValSerAspLeuGlnValSerGlyLeuPhePheAlaIleGly 254
 Db 66017 AATGTTGTACTGGGATGTTTTCAGATCTGAGAGGTGCTGGATTTGTTCTTTGCTATTGGT 66076
 QY 255 HisGluProAlaThrLysPheLeuGlyGlyGlnIleuGluLeuAspSerAspGlyTyrVal 274
 Db 66077 CATGAGCCAGCTACCGAAGTTTTTGGATGGCCAGCTTGAGCTTGATCAAGATGCTTATGTT 66136
 QY 275 GluThrLysProGlySerThrHisThrSerValLysGlyValPheAlaGlyAspVal 294
 Db 66137 GTGACCAAGCCAGGACTACTAAGACGACGGTGGTGGTGTATTTGCTGCTGGAGATGTT 66196
 QY 295 GlnAspLysLysTyrArgGlnAlaIleThrAlaAlaGlySerGlyCysMetAlaAlaLeu 314
 Db 66197 CAAGACAGAGACTATAGACAGGCCCATCACTGCTGCAGGAACTGGTTTGTACTCTTAACCTTG 66256
 QY 315 AspAlaGluHisTyr 319
 Db 66257 TATTTTTTACATTTC 66271

Search completed: May 5, 2004, 04:58:05
 Job time : 4095.73 secs

Percent Similarity: 85.54% Conservative: 27
 Best Local Similarity: 77.23% Mismatches: 43
 Query Match: 75.48% Indels: 4
 DB: 6 Gaps: 1

US-10-005-429-25 (1-331) x AX366997 (1-1021)

Qy 11 ThrArgIleCysIleIleGlySerGlyProAlaAlaHisThrAlaAlaIleTyrAlaAla 30
 Db 34 ACCCGCTCGATGCTGGCTCGCGCGGCTGCTCCACCGCGCGCATCTACGCGCC 93

Qy 31 ArgAlaGluLeuLysProValLeuPheGluGlyTyrMetAlaAsnAspIleAlaAlaGly 50
 Db 94 CGCGCGAGCTGAGCGGCTCTCTTCGAGGGCTGATGGCCACGACATCGCCCGGC 153

Qy 51 GlyGlnLeuThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThr 70
 Db 154 GCGCAGCTCACCAACACCGACGCTGAGAGACTTCCTCCCGGCTTCCTCCGAGGATCTC 213

Qy 71 GlyAlaAspLeuMetAspAsnCysArgAlaGlnSerLeuArgPheGlyThrAsnIleLeu 90
 Db 214 GCGTGGCTGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 273

Qy 91 SerGluThrValThrAlaValAspPheSerAlaCysProPheArgValSerAlaAspSer 110
 Db 274 ACCGACGCTGACCAAGGTGACTTCGAGACGCGCTTCAAGCTCTTCAACGACTCC 333

Qy 111 ThrThrValLeuAlaAspAlaValIleValAlaThrGlyAlaValAlaAargLeuHis 130
 Db 334 AGCGCATCTCGCGACGCGCTGATCTCGCATCGCGCGCGCTGCGCAAGTCTCTCC 393

Qy 131 PheProGlySer-----AspAlaTyrTyrAsnArgGlyIleSerAlaCysAla 146
 Db 394 TTCGTGGCTCGCGGAGTGTGCGGCGCTCTGGAACCGCGCATCTCGCGCTGGCT 453

Qy 147 ValCysAspGlyAlaAlaProIlePheArgAsnLysProIleAlaValIleGlyGly 166
 Db 454 GTGTGGAGCGCGCGCGCGCGCTTTCGCAACAGCGCGCTCGCTGTGATCGTGCGGA 513

Qy 167 AspSerAlaMetGluGluSerAsnPheLeuThrLysTyrGlySerHisValTyrIleIle 186
 Db 514 GACAGCGCATGGAGGAGCGCACTTCTCCACCAAGTACGCTCCAGGTGTATCATATC 573

Qy 187 HisArgAsnThrPheArgAlaSerIleValMetGlnAlaArgAlaLeuGluAsnPro 206
 Db 574 GACCGCGGAGCGCTTTCGCGCGCTTCCAGATCATGACGAGCGCGCGCTTCCAGCG 633

Qy 207 LysIleLysValLeuThrAspSerGluValValGluAlaTyrGlyAlaAsnGlyGly 226
 Db 634 AGATCGAGCTCATCTGGAGCTTCTCGCGTGGAGGCTTACGCGGAGCGCGCGGAC 693

Qy 227 ProLeuAlaGlyValLysValLysAsnLeuLeuAsnGlyGluValSerAspLeuGlnVal 246
 Db 694 GTGCTCGCGCGCTCAAGGTGAAGACGTTGACCGCGGACGCGCGCTTCCAGCTCA 753

Qy 247 SerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLysPheLeuGlyGlyGlnLeu 266
 Db 754 TCGCGCTCTTCTCGCGCATCGCGCATCGCGCGCGCGCATCGCGCGCGCGCGCTG 813

Qy 267 GluLeuAspSerAspGlyTyrValGluThrLysProGlySerThrHisThrSerValLys 286
 Db 814 GAGCTGATCTCGAGCGCTACGTGTGACCAAGCGCGGACCAACCGACCTTCGTGCT 873

Qy 287 GlyValPheAlaAlaGlyAspValGlnAspLysLysTyrArgGlnAlaIleThrAlaAla 306
 Db 874 GCGGTGTTCG 933

Qy 307 GlySerGlyCysMetAlaAlaLeuAspAlaGluHisTyrLeuGlnGluIleGlyAlaGln 326
 Db 934 GGCACGCGCTGATGCG 993

Qy 327 GluGlyLysSerAsp 331

994 CAGGCGAAGTCGAC 1008

Db

RESULT 14

LOCUS

ATTIREDB

A.thaliana mRNA for NADPH thioredoxin reductase.

223109

223109.1 GI:468525

NADPH thioredoxin reductase.

Arabidopsis thaliana (thale cress)

Arabidopsis thaliana

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE

1 (bases 1 to 1261)

Jacquot,J.P., Rivera-Madrid,R., Marinho,P., Kollarova,M., Le Marechal,P., Migninac-Maslow,M. and Meyer.Y.

Arabidopsis thaliana NADPH thioredoxin reductase. cDNA characterization and expression of the recombinant protein in Escherichia coli

J. Mol. Biol. 235 (4), 1357-1363 (1994)

JOURNAL

MEDLINE

94141931

3308900

REFERENCE

2 (bases 1 to 1261)

Jacquot,J., Rivera-Madrid,R., Marinho,P., Kollarova,M., Le Marechal,P., Migninac-Maslow,M. and Meyer.Y.

Arabidopsis thaliana NADPH thioredoxin reductase: cDNA characterization and expression of the recombinant protein in Escherichia coli

JOURNAL

REFERENCE

3 (bases 1 to 1261)

Meyer,Y.

Direct Submission

Submitted (24-JUN-1993) Yves Meyer, Labo de Physio et Biol Mol Vegetales, CNRS, URA 565, Av. de Villeneuve, PERPIGNAN, 66860, FRANCE

FEATURES

source

1..1261

/organism="Arabidopsis thaliana"

/mol_type="mRNA"

/db_xref="taxon:3702"

/tissue_type="silique"

/dev_stage="late flowering"

96..1094

/codon_start=1

/product="Thioredoxin reductase"

/protein_id="CAA80656.1"

/db_xref="GI:468526"

/db_xref="GOA:Q39243"

/db_xref="SWISS-PROT:Q39243"

/translation="MNGLETHRLCTIVGSGPAHTAAIYAARAEKPLLEFGMAMD IAPQQLNPPREPFPEGLVLELTFKQSERFGTTITETVTKVDFSPKPEP LFTQSKALADAVILACAVAKWLSFVSGEVLGGLWNRGISACVCDGAIPRNKPV LAVTGGSAMSEANFLT KYGSKVY IIDRDAFRASIMQORALSINPKIDIVNWSVV EAYGDERDLVGLKVNVTGDVSLKVSLEFPFAGHEPATKFLDGVLDSDGVVY TRGTTQTSVPGVPAAGVDQKKYRQAITAAGTGCMAALDAEHVLQELGSGQGSKD"

CDS

Alignment Scores:

Pred. No.: 9,86e-96 Length: 1261

Score: 1244.50 Matches: 245

Percent Similarity: 83.69% Conservative: 27

Best Local Similarity: 75.38% Mismatches: 48

Query Match: 72.82% Indels: 5

DB: 8 Gaps: 2

US-10-005-429-25 (1-331) x ATTIREDB (1-1261)

Qy 11 ThrArgIleCysIleIleGlySerGlyProAlaAlaHisThrAlaAlaIleTyrAlaAla 30

Db 120 ACAAGGCTCTGATCGTAGGAAGTGGCCAGCGGACACACAGCGCGGCGATTTACGAGCT 179

Qy 31 ArgAlaGluLeuLysProValLeuPheGluGlyTyrMetAlaAsnAspIleAlaAlaGly 50

```

submitted to Genbank.
FEATURES             Location/Qualifiers
     source            1..1433
                        /organism="Arabidopsis thaliana"
                        /mol_type="rRNA"
                        /db_xref="taxon:3702"
                        /chromosome="4"
                        /clone="RAF16-02-L06 (R50174)"
                        /ecotype="Columbia"
                        /note="This clone is in a modified pBluescript vector2
                        (lambda PS) as a BamHI/XhoI insert."
     gene              1..1433
                        /gene="At4g35460"
     5'UTR             1..73
                        /gene="At4g35460"
     misc_difference    4
                        /gene="At4g35460"
                        /note="compared to genomic sequence"
                        /replace="g"
                        74..1075
     CDS               /gene="At4g35460"
                        /codon_start=1
                        /evidence=experimental
                        /product="putative thioredoxin reductase (NADPH) 2"
                        /protein_id="AAO42318.1"
                        /db_xref="GI:28393813"
                        /translation="MNGLETRNTRLCIVGSPAAHTAAIYAARAEKLPFLPEGMAND
                        IAPGGUTTTVDNPGFPEGILGVELTDKPKOSRPGTTFTEVTVKVDFSSKEF
                        KLFDSXAILADAVILATGAVAKLSFVSGENGSGFWMRGISACVCDGAAPIFRNK
                        PLAVIGGDSAMEANETKYGSVYIIHRRDAFRASKIMQORALSNPKIDVFNWSSV
                        VEKGGDERDVLGLKVNVTGVDVSLKVSGLFPAIGHSEPAFKPLDGGVVELSDGVV
                        VTKGTTTQTSVPGVFAAGVDQDKYRQAIITAAGTGCMAALDABHYLQEIQSQQGSD"
     misc_difference    710
                        /gene="At4g35460"
                        /note="compared to genomic sequence resulting in an amino
                        acid sequence difference"
                        /replace="a"
                        1076..1433
     3'UTR            /gene="At4g35460"

ORIGIN
Alignment Scores:
Pred. No.:           1.3e-101          Length:           1433
Score:              1315.00           Matches:          254
Percent Similarity: 86.46%            Conservative:    27
Best Local Similarity: 78.15%          Mismatches:      40
Query Match:        76.95%            Indels:          4
DB:                  8                Gaps:            1

US-10-005-429-25 (1-331) x BF004322 (1-1433)
Qy 11 ThrArgIleCysIleIleGlySerGlyProAlaAlaHisThrAlaAlaIleTyzAlaAla 30
Db 98 ACAAGGCTCTGTATGTAGGAGTGGCCCGGCGGCACACACGCGCGGATTTACCGAGCT 157
Qy 31 ArgAlaGluLeuLysProValLeuPheGluGlyTrpMetAlaAsnAspIleAlaAlaGly 50
Db 158 AGGGGTGAACCTTAAACCTCTCTCTCTGGAAGATGGATGGTAAACGACATCGCTCCCGGT 217
Qy 51 GlyGlnLeuThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrMet 70
Db 218 GGTCAACTAAACACACCCCGACGTCGAGAAATTTCCCGGATTTCCGAGAGGTATCTC 277
Qy 71 GlyAlaAspLeuMetAspAsnCysArgAlaGlnSerLeuArgPheGlyThrAsnIleLeu 90
Db 278 GGAGTAGAGCTCACTGACAAATTCGTAAACAAATCGGAGCGATTCGGTACTACGATATT 337
Qy 91 SerGluThrValThrAlaValAspPheSerAlaCysProPheArgValSerAlaAspSer 110
Db 338 ACAGAGACGGTACCAAGAGTGGATTTCTTCGAAACCGTTTAAAGCTATTACAGATTTCA 397
Qy 111 ThrThrValLeuAlaAspAlaValIleValAlaThrGlyAlaValAlaAlaArgLeuHis 130

```

```

398 AAAGCCATTCTCGCTGACGCTGTGATTCTCGCTACTGGAGCTGTGGCTAAGCGCTTAGC 457
131 PheProGly-----SerAspAlaIleTrpAsnArgGlyIleSerAlaCysAla 146
458 TTGTTGGATCTGGTGAAGCTTCTGGAGGTTTCTGGAAACGCTGGAATCTCCGCTTGCT 517
147 ValCysAspGlyAlaAlaProIlePheArgAsnLysProIleAlaValIleGlyGly 166
518 GTTTCGACGAGCTCTCCGATATTCCGTAACAAACCTCTTCGGGTGATCGGTGAGGC 577
167 AspSerAlaMetGluGluSerAsnPheLeuThrLysTyrrGlySerHisValTyrrIle 186
578 GATTCAAGCAATGGAGAGCAAACTTCTTACAAATATGATCTAAAGTGTATATAATC 637
187 HisArgArgAsnThrPheArgAlaSerLysIleMetGlnAlaArgAlaLeuGluAsnPro 206
638 CATAGGAGAGATGCTTTTAGAGCGCTTAAGATTATGACGAGCGAGCTTTGTCTAATCCT 697
207 LysIleLysValLeuTrpAspSerGluValValGluAlaTyrrGlyAlaAsnGlyGly 226
698 AAGATTGATGTTTGGAACTGCTGTTGTGGAAGCTTATGGAGATGGAGAAAGAGAT 757
227 ProLeuAlaGlyValLysValLysAsnLeuLeuAsnGlyGluValSerAspLeuGlnVal 246
758 GTGCTTGGAGGATTGAAGTGAAGAATGTGCTTACCGGAGATGTTTCTGATTTAAAGTT 817
247 SerClyLeuPhePheAlaIleGlyHisGluProAlaThrLysPheLeuGlyGlnLeu 266
818 TCTGGATGTGTTCTGATGTGTCATGTCAGCCAGCTACCAAGTTTTCGATGTTGGTGT 877
267 GluLeuAspSerAspGlyTyrrValGluThrLysProGlySerThrHisThrSerValLys 286
878 GAGTTAGATTCCGATGCTTATGTTGTCAGGAGCTGTTACTACACAGACTAGCGTTCCC 937
287 GlyValPheAlaAlaGlyAspValGlnAspLysTyrrArgGlnAlaIleThrAlaAla 306
938 GAGATTTTTCGCTCGGGTGATGTTTCAGGATAAGAGTATAGGCAAGCCATCCTGCTGCA 997
307 GlySerGlyCysMetAlaAlaLeuAspAlaGluHisTyrrLeuGlnGluIleGlyAlaGln 326
998 GGAACCTGGTGATGGCGAGCTTTGGATGCAGAGCATTACTTACAAGAGATTGGATCTCAG 1057
327 GluGlyLysSerAsp 331
1058 CAAGGTAAGAGTGTAT 1072

RESULT 13
LOCUS AX366997 1021 bp DNA linear PAT 16-FEB-2002
DEFINITION Sequence 24 from Patent WO0198509.
ACCESSION AX366997
VERSION AX366997.1 GI:18698274
KEYWORDS Arabidopsis thaliana (thale cress)
SOURCE Arabidopsis thaliana
ORGANISM Arabidopsis thaliana
REFERENCE
 1 Lanahan,M.B., Desai,N.M. and Gasdaska,P.Y.
  Grain processing method and transgenic plants useful therein
  Patent: WO 0198509-A 24 27-DEC-2001;
  Syngenta Participations AG (CH)
FEATURES
  source
    1..1021
    /organism="Arabidopsis thaliana"
    /mol_type="unassigned DNA"
    /db_xref="taxon:3702"

ORIGIN
Alignment Scores:
Pred. No.:           1.1e-99          Length:           1021
Score:              1290.00           Matches:          251

```

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE
AUTHORS
Chang H.S., Chen, W., Cooper, B., Glazebrook, J., Goff, S.A., Hou, Y.M.,
Katagiri, F., Qian, S., Tao, Y., Whitham, S., Xie, Z., Zhu, T. and Zou, G.
TITLE
JOURNAL
Plant genes involved in defense against pathogens
Patent: WO 0300898-A 148 03-JAN-2003;
Syngenta Participations AG (CH)

FEATURES
source
Location/Qualifiers
1. 1152
/organism="Arabidopsis thaliana"
/mol_type="unassigned DNA"
/db_xref="taxon:3702"

ORIGIN
Alignment Scores:
Pred. No.: 1.85e-103 Length: 1152
Score: 1335.50 Matches: 258
Percent Similarity: 86.65% Conservative: 34
Best Local Similarity: 76.56% Mismatches: 36
Query Match: 78.15% Indels: 9
DB: 6 Gaps: 2

US-10-005-429-25 (1-331) x AX651358 (1-1152)

QY 4 SerAlaAlaProLeu-----ArgThrArgIleCysIleIleGlySer 18
DB 139 TCGCCCGCGCGCGTGCATCGAAGAACTCAGAAACCCAGGTTTCATCGTCGGAAGT 198

QY 19 GlyProAlaAlaHisThrAlaAlaIleTyrAlaAlaArgAlaGluLeuLysProValLeu 38
DB 199 GGCACGACGACACACGCGCGCGATCTATCGATCGAGCGGAGCTTAAGCCCTCTCTC 258

QY 39 PheGluGlyTrpMetAlaAsnAspIleAlaAlaGlyGlyGlnLeuThrThrThrAsp 58
DB 259 TTCAGAGGATGGATGGGTACGACGATCGCTCCCGCGGTCAATTAATACAAACCGAC 318

QY 59 ValGluAsnPheProGlyPheProAsnGlyIleMetGlyAlaAspLeuMetAspAsnCys 78
DB 319 GTCGAAACCTCCCTGGGTTCCCTGAGGATTTCTCGTATTGATATCGTTGAGAAATTC 378

QY 79 ArgAlaGlnSerLeuArgPheGlyThrAsnIleLeuSerGluThrValThrAlaValAsp 98
DB 379 AGAAACCAATCGGAGAGATTGGAACTACCATCTTCACGGAACCTGTAAACAAAGTTGAT 438

QY 99 PheSerAlaCysProPheArgValSerAlaAspSerThrThrValLeuAlaAspAlaVal 118
DB 439 TTCTCATCGAAACCGTTTAACTATTTCACCTGATTCGAGAACTGTCTCGCTGATTCGTA 498

QY 119 IleValAlaThrGlyAlaValAlaAlaArgArgLeuHisPheProGlySer----- 134
DB 499 ATCAATTTCTAGAGCTGTGTAAACGCTTACGCTTACGATCTGCTGAGGTAAT 558

QY 135 AspAlaTyrTrpAsnArgGlyIleSerAlaCysAlaValCysAspGlyAlaAlaProIle 154
DB 559 GGTGGTTTGGATCGGTGATCTCGCTGCTGTGCTGTTGGACGAGGCTGCTCGATT 618

QY 155 PheArgAsnLysProIleAlaValIleGlyGlyCysSerAlaMetGluGluSerAsn 174
DB 619 TTTAGGAATAAGCCTCTGTGGTTATTGGTGGTGGTGAATTCAGCTATGGAGGAGCGAAT 678

QY 175 PheLeuThrLysTyrGlySerHisValTyrIleIleHisArgArgAsnThrPheArgAla 194
DB 679 TTTCTGACTAAGTATGATCTAAGGTTTATATTATTCATAGGAGGATGATGTTTAGGCG 738

QY 195 SerLysIleMetGlnAlaArgAlaLeuGluAsnProLysIleLysValLeuTrpAspSer 214
DB 739 TCTAAGATTATCGACGACAGAGCTTGTCTAACCCCTAAGATTGAAGTATTTGGAATCT 798

QY 215 GluValValGluAlaTyrGlyAlaAsnGlyCysProLeuAlaGlyValLysValLys 234
DB 799 GCCGTGGTGGAGCGTATGGTGTGAAATGGACGCTGTTCTCTGGAGGATTTGAAGGTAAG 858

QY 235 AsnLeuLeuAsnGlyGluValSerAspLeuGlnValSerGlyLeuPhePheAlaIleGly 254
DB 859 AATGTTGTTACTGGGGATGTTTCAGATCTGAGGTTCTCGATGTTCTTCTTATGTT 918

QY 255 HisGluProAlaThrLysPheLeuGlyGlnLeuGluLeuAspSerAspGlyTyrVal 274
DB 919 CATGAGCCAGCTACGAGTTTGGATGGGACCTTGAGCTTGATGAAGATGTTTANGTT 978

QY 275 GluThrLysProGlySerThrHisThrSerValLysGlyValPheAlaAlaGlyAspVal 294
DB 979 GTGACCAAGCCAGGCTACTACTAAGACGAGCGTGGTTGGTGTATTTGCTGCTGGAGATGTT 1038

QY 295 GluAspLysLysTyrArgGlnAlaIleThrAlaAlaGlySerGlyCysMetAlaAlaLeu 314
DB 1039 CAAGACAAGAAATATAGACAGGCGCATCTGTCGAGAACTGGGTGTCATGGCGGCAATTG 1098

QY 315 AspAlaGluHisTyrLeuGlnGluIleGlyValAlaGlnGlyLysSerAsp 331
DB 1099 GATGCAGAGCATTTACTTACAGAGATTTGATCTTCAGAGGGTAAAGATGAT 1149

RESULT 12
BT004322
LOCUS
DEFINITION
BT004322 1433 bp mRNA linear PLN 14-FEB-2003
thioredoxin reductase (NADPH) 2 (At4g35460) mRNA, complete cds.
ACCESSION
BT004322.1 GI:28393818
VERSION
FLI CDNA.
KEYWORDS
Arabidopsis thaliana (thale cress)
SOURCE
Arabidopsis thaliana
ORGANISM
Arabidopsis thaliana
REFERENCE
1 (bases 1 to 1433)
Yamada, K., Chan, M.M., Chang, C.H., Dale, J.M., Hsuan, V.W., Lee, J.M.,
Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Wong, C., Wu, H.C.,
Yu, G., Yuan, S., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y.,
Ishida, J., Jones, T., Kamiya, A., Kawai, J., Kim, C.J., Narusaka, M.,
Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shinn, P.,
Southwick, A., Tripp, M.G., Wu, T., Shinozaki, K., Davis, R.W.,
Ecker, J.R. and Theologis, A.
AUTHORS
Arabidopsis Full Length cDNA Clones
Unpublished
2 (bases 1 to 1433)
Yamada, K., Chan, M.M., Chang, C.H., Dale, J.M., Hsuan, V.W., Lee, J.M.,
Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Wong, C., Wu, H.C.,
Yu, G., Yuan, S., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y.,
Ishida, J., Jones, T., Kamiya, A., Kawai, J., Kim, C.J., Narusaka, M.,
Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shinn, P.,
Southwick, A., Tripp, M.G., Wu, T., Shinozaki, K., Davis, R.W.,
Ecker, J.R. and Theologis, A.
REFERENCE
Submitted (14-FEB-2003) Plant Gene Expression Center, 800 Buchanan
Street, Albany, CA 94710, USA
RIKEN Genomic Sciences Center (GSC) members carried out the
collection and clustering of RAPL cDNAs (RAPL cDNA: "RIKEN
Arabidopsis Full-length cDNA"): Seki, M., Narusaka, M., Ishida, J.,
Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J.,
Hayashizaki, Y. and Shinozaki, K.
TITLE
JOURNAL
Direct Submission
COMMENT
The Salk, Stanford, PGEC (SSP) Consortium members carried out the
sequencing and annotation of the RAPL cDNAs: Yamada, K., Chan, M.M.,
Chang, C.H., Dale, J.M., Hsuan, V.W., Lee, J.M., Onodera, C.S.,
Quach, H.L., Tang, C.C., Toriumi, M., Wong, C., Wu, H.C., Yu, G.,
Yuan, S., Chen, H., Cheuk, R., Jones, T., Kim, C.J., Nguyen, M.,
Palm, C.J., Shinn, P., Southwick, A., Tripp, M.G., Wu, T., Davis, R.W.,
Ecker, J.R. and Theologis, A.
Yamada, K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed equally to
this work. Shinozaki, K. (RIKEN GSC) and Theologis, A. (SSP/PGEC)
contributed equally to this work as PIs.
Annotation based on July 2002 version of the Arabidopsis genome


```

Qy 161 AlaValIleGlyGlyGlyAspSerAlaMetGluSerAsnPheLeuThrLysTyrGly 180
Db 481 GCGTCATCGCGGCGGCGAGTCCGCCATCGAGGAGTCCAACTTCCTCACCAAGTACGCC 540
Qy 181 SerHisValTyrIleLeuHisArgAsnThrPheArgAlaSerLysIleMetGlnAla 200
Db 541 TCCCATGTGTACATCATCCACCGCGGACACACCTTCGCGCGCTCCCAAGATCATGACGCC 600
Qy 201 ArgAlaLeuGluAsnProLysIleLysValLeuTyrAspSerGluValValGluAlaTyr 220
Db 601 AGGCGTGTGTCAACCCCAAGATCCAGGTTTCTGGGACTCTGAGGTCTGCGAGCCCTAC 660
Qy 221 GlyGlyAlaSerGlyGlyProLeuAlaGlyValLysValLysAsnLeuLeuAsnGlyGlu 240
Db 661 GCGCGC---GAGCGCTCGAGGCTCATGGCTGCTGCTCAAG----- 699
Qy 241 ValSerAspLeuGlnValSerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLys 260
Db 700 -----GTTCTCGTCTCTCTTCGCCATCGGACATGATCAACCGGCGACGAG 744
Qy 261 PheLeuGlyGlyGlnLeuGluLeuAspSerAspGlyTyrValGluThrLysProGlySer 280
Db 745 TTTCTCGCGCGGAGCTTGAAGTGGTATGATGGTATGTTGGCCACCAAGCCAGGCTCC 804
Qy 281 ThrHisThrSerValLysGlyValPheAlaIleGlyValAspValGlnAspLysLysTyrArg 300
Db 805 ACGCACACCAAGTGTGAAGGGGGTCTTGTCTGCTGGGATGTGCAGGACAAAGATATCGC 864
Qy 301 GlnAlaIleThrAlaAlaGlySer-----GlyCys 310
Db 865 CAGGCTATTACTCGCGCTGGATCAGATCAGTCCGCTTCATGGGTTC 912

RESULT 10
AX507791 1152 bp DNA linear PAT 27-SBP-2002
LOCUS
DEFINITION Sequence 2486 from Patent WO0216655.
ACCESSION AX507791
VERSION AX507791.1 GI:23389028
KEYWORDS
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsia.
1
REFERENCE Harper, J.F., Krops, J., Wang, X. and Zhu, T.
AUTHORS Stress-regulated genes of plants, transgenic plants containing
TITLE same, and methods of use
JOURNAL Patent: WO 0216655-A 2486 28-FEB-2002;
The Scripps Research Institute (US) ; Syngenta Participations AG
(CH)
FEATURES
source Location/Qualifiers
1..1152
/organism="Arabidopsis thaliana"
/mol_type="unassigned DNA"
/db_xref="taxon:3702"
ORIGIN
Alignment Scores:
Pred. No.: 1..85e-103 Length: 1152
Score: 1335.50 Matches: 258
Percent Similarity: 86.85% Conservative: 34
Best Local Similarity: 76.56% Mismatches: 36
Query Match: 78.15% Indels: 9
DB: 6 Gaps: 2

US-10-005-429-25 (1-331) x AX507791 (1-1152)
Qy 4 SerAlaAlaProLeu-----ArgThrArgIleCysIleIleGlySer 18
Db 139 TCCGCGCGCGCGCGCGATCGATCGAAGTCAAAACCAAGGTTTCATGCTCGCGAAGT 198
Qy 19 GlyProAlaAlaHisThrAlaAlaIleTyrAlaAlaArgAlaGluLeuLysProValLeu 38

```

```

Db 199 GGACACGACGACACACACGCGCGATCTATGATCATGAGACGCGAGCTTAAGCCTCTCTC 258
Qy 39 PheGluGlyTyrMetAlaAsnAspIleAlaAlaGlyGlyGlnLeuThrThrThrAsp 58
Db 259 TTCGAAGGATGATGCTAACACATCTGCTCCGCGGCTCAATTAATCAACAACCGAC 318
Qy 59 ValGluAsnPheProGlyPheProAsnGlyIleMetGlyAlaAspLeuMetAspCys 78
Db 319 GTCGAAAACCTTCCTCGGTTCCCTGAAGGTATTCTCGGTATTGATATCGTTGAGAAATTC 378
Qy 79 ArgAlaGlnSerLeuArgPheGlyThrAsnIleLeuSerGlnThrValThrAlaValAsp 98
Db 379 AGAAACATTCGAGAGATTTGAACATACGATCTCCGGAACACTGTTAACAAAGTTGAT 438
Qy 99 PheSerAlaCysProPheArgValSerAlaAspSerThrThrValLeuAlaAspAlaVal 118
Db 439 TTTCTCATCGAAAACCGTTTAAGCTATTCACTGATTTCGAGAACTGTTCTCGCTGATTCGTA 498
Qy 119 IleValAlaThrGlyAlaValAlaAlaArgArgGlnLeuHisPheProGlySer----- 134
Db 499 ATCATTTCTACTGAGAGCTGTTGCTAACGCTTTAGCTTCTCATGATCTCGTGAAGTAAT 558
Qy 135 AspAlaTyrTyrAsnArgGlyIleSerAlaCysAlaValCysAspGlyAlaAlaProIle 154
Db 559 GGTGGTTTTTGGATCTGCTATCTCGCTTGTGCTGTTTGGACGAGAGCTGCTCCGATT 618
Qy 155 PheArgAsnLysProIleAlaValIleGlyGlyAspSerAlaMetGluLysSerAsn 174
Db 619 TTTAGGAATAAGCCTCTTGTGGTTATTGTTGGTGGTGGATTTCAGCTATGAGGAAGCGAAT 678
Qy 175 PheLeuThrLysTyrGlySerHisValTyrIleIleHisArgArgAsnThrPheArgAla 194
Db 679 TTTCTGACTAAGTATGATCTAAGGTTTATATTATTATAGGAGGATACGTTTAGGGCG 738
Qy 195 SerLysIleMetGlnAlaArgAlaLeuGluAsnProLysIleLysValLeuThrAspSer 214
Db 739 TCTAAGATTATGCAGCAGAGAGCTTTGTCTCTAAGCTCTGAAGTGTCTGCTGCTATTGGT 798
Qy 215 GluValValGluAlaTyrGlyGlyAlaAsnGlyGlyProLeuAlaGlyValLysValLys 234
Db 799 GCCGTGTTGAGCGGATGATGATGAATGAGCGTGTCTTCGAGGATGAGGTTGAG 858
Qy 235 AsnLeuLeuAsnGlyGluValSerAspLeuGlnValSerGlyLeuPheAlaIleGly 254
Db 859 AATGTTGTACTCGGCGATGTTTCAGATCTGAAGTGTCTGCTGCTGCTGCTATTGGT 918
Qy 255 HisGluProAlaThrLysPheLeuGlyGlnLeuGluLysSerAspGlyTyrVal 274
Db 919 CATGAGCCAGCTACGAAAGTTTTTGGATGGCGAGCTTGAGCTTGATGAAGATGTTATGT 978
Qy 275 GluThrLysProGlySerThrHisThrSerValLysGlyValPheAlaAlaGlyAspVal 294
Db 979 GTGACCAAGCCAGGTACTACTAAGACGCGGTGTTGGTGTATTCTGCTGAGATGTT 1038
Qy 295 GlnAspLysIleTyrArgGlnAlaIleThrAlaAlaGlySerGlyCysMetAlaAlaLeu 314
Db 1039 CAAGACAAGAAGTATAGACAGGCCCATCTGCTGCGAGGAGTGGGTGCGATGCGCGCATG 1098
Qy 315 AspAlaGluHisTyrLeuGlnGluIleGlyAlaGlnGluGlyLysSerAsp 331
Db 1099 GATGCGAGCATTTACTTACAGAGATTGATCTTCAGAGGGGTAGAGTGTAT 1149

RESULT 11
AX651358
LOCUS
DEFINITION Sequence 148 from Patent WO0300898.
ACCESSION AX651358
VERSION AX651358.1 GI:29154176
KEYWORDS
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

```



```

Db      1246  ACGCACACCACTGTGTCAGGGGCTCTTCTGCTGGGATGTGCAGGACAGAGTATCGC 1305
Qy      301  GlnAlaIleThrAlaAlaGlySerGly 309
Db      1306  CAGGCTATTACTGCGCTGGATCAGGT 1332

RESULT 7
AP005477
LOCUS    AP005477                131980 bp    DNA        linear    HTG 28-JUN-2002
DEFINITION Oryza sativa (japonica cultivar-group) chromosome 6 clone
OSUNBB0039F24, ** SEQUENCING IN PROGRESS ***
ACCESSION AP005477
VERSION    AP005477.1 GI:21624397
KEYWORDS   HTG; HTGS PHASE2.
SOURCE     Oryza sativa (japonica cultivar-group)
ORGANISM   Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE
1  Sasaki, T., Matsumoto, T. and Katayose, Y.
   Oryza sativa nipponbare (GA3) genomic DNA, chromosome 6, BAC
   clone OSUNBB0039F24
   Published Only in Database (2002)
2  (Bases 1 to 131980)
   Sasaki, T., Matsumoto, T. and Katayose, Y.
   Direct Submission
   Submitted (26-JUN-2002) Takuji Sasaki, National Institute of
   Agrobiological Sciences, Rice Genome Research Program; Kamondai
   2-1-2, Tsukuba, Ibaraki 305-8602, Japan
   (E-mail: tsasakion@affrc.go.jp, URL: http://rnp.dna.affrc.go.jp/,
   Tel: 81-298-38-7441, Fax: 81-298-38-7468)
   NOTE: It currently consists of 1 contigs. Gaps between the contigs
   are represented as runs of N. The order of the pieces is believed
   to be correct as given, however the sizes of the gaps between them
   are based on estimates that have provided by the submitter. This
   sequence will be replaced by the finished sequence as soon as it is
   available and the accession number will be replaced.
   * NOTE: This is a 'working draft' sequence.
   * This sequence will be replaced
   * by the finished sequence as soon as it is available and
   * the accession number will be preserved.

FEATURES
    source
        1..131980
            /organism="Oryza sativa (japonica cultivar-group)"
            /mol_type="genomic DNA"
            /cultivar="Nipponbare"
            /db_xref="taxon:39947"
            /chromosome="6"
            /clone="OSUNBB0039F24"

ORIGIN
Alignment Scores:
Pred. No.:      1.04e-107      Length:      131980
Score:          1416.00      Matches:      270
Percent Similarity: 94.53%      Conservative: 24
Best Local Similarity: 86.82%      Mismatches:  17
Query Match:      82.86%      Indels:      0
DB:              2              Gaps:        0

US-10-005-429-25 (1-331) x AP005477 (1-131980)

Qy      1  MetGluGlySerAlaAlaAlaProLeuArgThrArgIleCysIleIleGlySerGlyPro 20
Db      82633  ATGGAGGAGGCGCGCGCGCGCGCTGCGCGCGCGCGTGCATCATCGGAGCGCGCGCG 82692

Qy      21  AlaAlaHisThrAlaAlaIleTyrAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 40
Db      82693  GCGGCGCACACGCGCGCGCTTACGCGCGCGCGCGCGAGCTCAAGCGCGCTCTTCGAG 82752

Qy      41  GlyTrpMetAlaAsnAspIleAlaAlaGlyGlnLeuThrThrThrThrThrThrThrThrThr 60
Db      82753  GGTCTCTCGGCACGACGATCGCGCGCGCGCGCGAGCTCACACCGACCGAGTCGAG 82812

```

```

Qy      61  AsnPheProGlyPheProAsnGlyIleMetGlyAlaAspLeuMetAspAsnCysArgAla 80
Db      82813  AACTTCCGGGCTTCCCGGCGGACATCTCTGGCGCGGACCTCATGGACCGCTCCGCGCC 82872

Qy      81  GlnSerLeuArgPheGlyThrAsnIleLeuSerGlyThrValThrAlaValAspPheSer 100
Db      82873  CAGTCCGTGGCTTCGGACCCAGGATCTCACCGAGACCGTCAACCGCGTCCGACCTCTCG 82932

Qy      101  AlaCysProPheArgValSerAlaAspSerThrThrValLeuAlaAspAlaValIleVal 120
Db      82933  TCCGCGCCCTTCCGCGTCCGCTCCGCGACACCGCTGTCGACCGCGCGTGGTCTGTCG 82992

Qy      121  AlaThrGlyAlaValAlaAlaArgArgLeuHisPheProGlySerAspAlaTyrTrpAsnArg 140
Db      82993  GCCACGGCGCGCTCCGCGCGCGCTCCATTCGCGGCTCCGACGATCTTCGACCGCGC 83052

Qy      141  GlyIleSerAlaCysAlaValCysAspGlyAlaAlaProIlePheArgAsnLysProIle 160
Db      83053  GGCATCTCCGCTCCGCGCTCCGCGCGCGCTCCGCGCGCGCTCCATCTTCGCGAACAGCC 83112

Qy      161  AlaValIleGlyGlyValAspSerAlaMetGluGluSerAsnPheLeuThrLysTyrGly 180
Db      83113  GCGTCTGTCGCGCGCGCGGACTCCGCGATGCGAGCGCGCGCTTCCTCACCAAGATCAGC 83172

Qy      181  SerHisValTyrIleIleHisArgArgAsnThrPheArgAlaSerLysIleMetGlnAla 200
Db      83173  TCCGCGCTCTACATCATCCACCGCGCGCTTCGCGCGCTCCAGATCATGACGCGC 83232

Qy      201  ArgAlaLeuGluAsnProLysIleLysValLeuTrpAspSerGluValValGluAlaTyr 220
Db      83233  CGGCGCTCTCCAAACCCCAAGATCCAGGTCTCTGGGACTCCGAGGTCTCGAGGGGTAC 83292

Qy      221  GlyGlyAlaAsnGlyGlyProLeuAlaGlyValLysValLysAsnLeuLeuAsnGlyGlu 240
Db      83293  GCGCGCGCGCGCGCTCGTTCGTTGGCGGCGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 83352

Qy      241  ValSerAspLeuGlnValSerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLys 260
Db      83353  GTCTCCGACCTCCAGGTTCGCGCGCTCTTCTTCGCCATTTGGACGACGCGCGGACAAAG 83412

Qy      261  PheLeuGlyGlyGlnLeuGluLeuAspSerAspGlyTyrValGluThrLysProGlySer 280
Db      83413  TTCTCGCGCGCGCGCTCGAGCTGGACTCGATGGCTATGTCGTGACCAAGCGCGCTCC 83472

Qy      281  ThrHisThrSerValLysGlyValPheAlaAlaGlyAspValGlnAspLysTyrArg 300
Db      83473  ACTCACACGACGCTCAAGGAGTCTTCGCGCGCGGTGATGTTCCAGGACAGAGTATCGC 83532

Qy      301  GlnAlaIleThrAlaAlaGlySerGlyCysMet 311
Db      83533  CAGGCCATTACTCGCGCGGATCAGGTATACTA 83565

RESULT 8
AX654214
LOCUS    AX654214                1130 bp    DNA        linear    PAT 22-MAR-2003
DEFINITION Sequence 4084 from Patent WO03000898.
ACCESSION AX654214
VERSION    AX654214.1 GI:29157028
KEYWORDS
SOURCE     Oryza sativa
ORGANISM   Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE
1  Chang, H.S., Chen, W., Cooper, B., Glazebrook, J., Goff, S.A., Hou, Y.M.,
   Katagiri, F., Quan, S., Tao, Y., Whitham, S., Xie, Z., Zhu, T. and Zou, G.
   Plant genes involved in defense against pathogens
   Patent: WO 0300898-A 4084 03-JAN-2003;
   Syngenta Participations AG (CH)
   Location/Qualifiers
       source
           1..1130

```

```

Db 99686 GGCTGGCTGCCAACGACATCGCGGGGGGGGCGAGCTCACCACCACCGAGCTCGAG 99627
Qy 61 AsnProGlyPheProAsnGlyIleMetGlyAlaAspLeuMetAspLeuCysArgAla 80
Db 99626 AACTTCCCGGGTTCCCGAGGGGATCTCTCGGGGAGGCTCATGGATCGTCCCGCGC 99567
Qy 81 GlnSerLeuArgPheGlyThrAniLeuSerGluThrValThrAlaValAspPheSer 100
Db 99566 CAGTCTCTCCGGTTGGCACCAGCATCATCTCGAGACCGTCAACGGGTCGATCTCTCC 99507
Qy 101 AlaCysProPheArgValSerAlaAspSerThrThrValLeuAlaAspAlaValIleVal 120
Db 99506 GCCCGCCCTTCCGCGTCCGCTCCGATCCACACCGTCTCGCCGAGCGCGTCTCGTC 99447
Qy 121 AlaThrGlyAlaValAlaArgAspLeuHisPheProGlySerAspAlaValTTPAsnArg 140
Db 99446 GCACCGGAGCGCGTCCCGCGGACATCTCACTTCGCGGCTCCGAGCTTACTGGAACCGC 99387
Qy 141 GlyLeuSerAlaCysAlaValCysAspGlyAlaAlaProIlePheArgAsnLysProIle 160
Db 99386 GGCATCTCCGCTCGCGTCTCGGACCGGCGCGCCCAATCTTCAGGAACAACCCATC 99327
Qy 161 AlaValIleGlyGlyGlyAspSerAlaMetGluGluSerAsnPheLeuThrLysTyrGly 180
Db 99326 GCGTCTATCGCGCGCGGCGGACTCCGCACTGAGAGAGTCCAACTTCTCACCAGTACGGC 99267
Qy 181 SerHisValTyrIleIleHisArgArgAsnThrPheArgAlaSerLysIleMetGlnAla 200
Db 99266 TCCATGTGTATCATCATCCACCGCGCAACACCTTCGCGCTCCCAAGATCATGACGGCC 99207
Qy 201 ArgAlaLeuGluAsnProLysIleLysValLeuThrAspSerGluValValGluAlaTyr 220
Db 99206 AGGGCGTTGTCAAAACCCCAAGATCCAGGTTTCTCGGACTCTGAGTCTCGGAGGCTTAC 99147
Qy 221 GlyGlyAlaAsnGlyGlyProLeuAlaGlyValLysValLysAsnLeuLeuAsnGlyGlu 240
Db 99146 GCGCGGAGGGTGGAGTCCATTTGGTGTGTCAGGTGAAGAACTTGTACTTGGGAAG 99087
Qy 241 ValSerAspLeuGlnValSerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLys 260
Db 99086 ATCTCGACCTTCAGGTGTCGGTCTCTTCTTCCCATCGGACATGAACCGGCGAGAG 99027
Qy 261 PheLeuGlyGlyGlnLeuGluLeuAspSerAspGlyTyrValGluThrLysProGlySer 280
Db 99026 TTTCTCGCGCGGAGCTTGAAGTTCGATGCTGATGGGTATGTGCCACCAAGCAGGCTCC 98967
Qy 281 ThrHisThrSerValLysGlyValPheAlaAlaGlyAspValGlnAspLysTyrArg 300
Db 98966 AGGCACCCAGTGTGAAGGGGTCTTTGCTGTGGGGATGTGCAGCAAGAAGTATCGC 98907
Qy 301 GlnAlaIleThrAlaAlaGlySerGly 309
Db 98906 CAGGCTATTACTGCCGCTGATCAGT 98880

RESULT 6
LOCUS AX366999 1560 bp DNA linear PAT 16-FEB-2002
DEFINITION Sequence 26 from Patent WO0198509.
ACCESSION AX366999
VERSION AX366999.1 GI:18698275
KEYWORDS Oryza sativa
SOURCE Oryza sativa
ORGANISM Oryza sativa
REFERENCE 1
AUTHORS Lanahan, M.B., Desai, N.M. and Gasdaska, P.Y.
TITLE Grain processing method and transgenic plants useful therein
JOURNAL Patent: WO 0198509-A 26 27-DEC-2001;
SYNOPSIS Syngenta Participations AG (CH)
FEATURES
source
1. .1560

```

```

/organism="Oryza sativa"
/mol_type="unassigned DNA"
/db_xref="taxon:4330"

ORIGIN
Alignment Scores:
Pred. No.: 2,54e-115 Length: 1560
Score: 1478.00 Matches: 282
Percent Similarity: 96.12% Conservative: 15
Best Local Similarity: 91.28% Mismatches: 12
Query Match: 86.48% Indels: 0
DB: 6 Gaps: 0

US-10-005-429-25 (1-331) x AX366999 (1-1560)
Qy 1 MetGluGlySerAlaAlaAlaProLeuArgThrArgIleCysIleIleGlySerGlyPro 20
Db 406 ATGGAGGGATCCCGCGGGCGCGCTCCGACCGCGCTGTGCATCATCGGAGCGGGCGC 465
Qy 21 AlaAlaHisThrAlaAlaIleTyrAlaAlaArgAlaGluLeuLysProValLeuPheGlu 40
Db 466 TCGCGGCACACGCGCGGATCTACGCGCGCGCGGAGCTCAAGCGCGTCTCTTCGAG 525
Qy 41 GlyTyrMetAlaAsnAspIleAlaIleGlyGlnLeuThrThrThrThrThrThrThr 60
Db 526 GCGTGGCTCGCCCAACGACATCGCGGGGGGCGGAGCTCACCACCACCGACGTCGAG 585
Qy 61 AsnPheProGlyPheProAsnGlyIleMetGlyAlaAlaAspLeuMetAspAsnCysArgAla 80
Db 586 AACTTCCCGGGTCTCCCGAGGGGATCTTCGCGCGGAGCTCATGGATCGGTGCGCGCC 645
Qy 81 GlnSerLeuArgPheGlyThrAsnIleLeuSerGluThrValThrAlaValAspPheSer 100
Db 646 CAGTCTCTCGGTTCCGACCAACGATCATCTCCGAGACGCTCACCAGCGTCCGCTCTCC 705
Qy 101 AlaCysProPheArgValSerAlaAspSerThrThrValLeuAlaAspAlaValIleVal 120
Db 706 GCGCGCGCTTCCGGTGGCTTCCGACTCCACACCGTGTGCGCGAGCGCGTCTCGTCTC 765
Qy 121 AlaThrGlyAlaValAlaArgArgLeuHisPheProGlySerAspAlaTyrTrpAsnArg 140
Db 766 GCACCGCGCGCTCGCGCGGACTCCACTTCGCGGCTCCGAGCGCTACTTGGAAACCGC 825
Qy 141 GlyIleSerAlaCysAlaValCysAspGlyAlaAlaProIlePheArgAsnLysProIle 160
Db 826 GGCATCTCAGCTCGCGCTCTCGAGCGGGCGCGCCCAATCTTCAGGAACAACCCATC 885
Qy 161 AlaValIleGlyGlyAspSerAlaMetGluGluSerAsnPheLeuThrLysTyrGly 180
Db 886 GCGTCTATCGCGCGGCGACTCCGCCATGGAGGAGTCCAACTTCTCACCAGTACGCGC 945
Qy 181 SerHisValTyrIleIleHisArgArgAsnThrPheArgAlaSerLysIleMetGlnAla 200
Db 946 TCCCATGTGTATCATCATCCCGCGCAACACTTTCGCGGCTCCAAAGATCATGAGGCGC 1005
Qy 201 ArgAlaLeuGluAsnProLysIleLysValLeuThrAspSerGluValValGluAlaTyr 220
Db 1006 AGGGGCTTGTCAAAACCCCAAGATCCAGGTTTCTGGGACTCTGAGGTCTCGAGGCTTAC 1065
Qy 221 GlyGlyAlaAsnGlyGlyProLeuAlaGlyValLysValLysAsnLeuLeuAsnGlyGlu 240
Db 1066 GCGCGGAGGGTGGAGGTCCATTTGGCTGTGTCAAGGTGAAGAACTTGGTTACTGGGAG 1125
Qy 241 ValSerAspLeuGlnValSerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLys 260
Db 1126 ATCTCGACCTTCAAGTGTCTCGGTCTCTTCTTGGCATCGGACATGAACCGGCGAGAG 1185
Qy 261 PheLeuGlyGlyGlnLeuLeuLeuAspSerAspGlyTyrValGluThrLysProGlySer 280
Db 1186 TTTCTCGCGCGGAGCTTGAAGTGTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 1245
Qy 281 ThrHisThrSerValLysGlyValPheAlaAlaGlyAspValGlnAspLysTyrArg 300

```

Db 818 TTCTCGCCGACAGCTCGAGCTCGACTCCGAGGGGTACGTGGCCACCAAGCCGGGCTCC 87

Qy

Qy 41 GlyTrpMetAlaAsnAspIleAlaAlaGlyGlyGlnLeuThrThrThrAspValGlu 60

Qy	21	AlaAlaHisThrAlaAlaIleIleValAlaAlaArgAlaGluLeuLysProValLeuPheGlu	40
Db	184	TCGGCGCACACGGCGCGCATCTACGCCCGCGCGCGAGCTCAAGCCCGTCTTCGAG	243
Qy	41	GlyTyrMetAlaAenAspIleAlaAlaGlyGlyGlnLeuThrThrThrAspValGlu	60
Db	244	GGCTGGCTCGCCAAACGACATCGCGCGGGGGCGCAGCTCACCAACACCGAGCTCGAG	303
Qy	61	AspPheProGlyPheProAsnGlyIleMetGlyAlaAspLeuMetAspAsnCysArgAla	80
Db	304	AACTTCCGGGGTTCCCGAGGGGATCTCCGGCGCGAGCTCATGGATCGTGGCGGCC	363
Qy	81	GlnSerLeuArgPheGlyThrAsnIleLeuSerGluThrValThrAlaValAspPheSer	100
Db	364	CAGTCCCTCCGGTTCCGACCATCTCCGAGACCGGTCAACCGGGTCGACTTCTCC	423
Qy	101	AlaCysProPheArgValSerAlaAspSerThrThrValLeuAlaAspAlaValIleVal	120
Db	424	GCCGCCCTTCCGGTGGCTCCGATCTCACACCGTGTCTCGCGAGCGCGTGTGTCTC	483
Qy	121	AlaThrGlyAlaValAlaAlaArgLeuHisPheProGlySerAspAlaTyrTTPAsnArg	140
Db	484	GCCACCGCGCGTGGCGCGGACTCCACTTCCGCGGCTCCGACGCTACTTGAACCGC	543
Qy	141	GlyIleSerAlaCysAlaValCysAspGlyAlaAlaProIlePheArgAsnLysProIle	160
Db	544	GGCATCTCCGCTCGCGCGTCTGGACGGGGCCGCCCAATCTTCAGAACCAACCCATC	603
Qy	161	AlaValIleGlyGlyAspSerAlaMetGluGlnSerAsnPheLeuThrLysTyrGly	180
Db	604	GCGGTATCCGCGCGCGCATCCGCCATCGAGGAGTCCAATCTCTCTCAACAGTACGGC	663
Qy	181	SerHisValTyrIleIleHisArgArgAsnThrPheArgAlaSerLysIleMetGlnAla	200
Db	664	TCCCATGTGTACATCATCCACCGCGCGCAACACTTCCGGCGCTTCCAAGATCATCGAGGC	723
Qy	201	ArgAlaLeuGluAsnProLysIleLysValLeuTTPAspSerGluValValGluAlaTyr	220
Db	724	AGGGGTGTCAACCCCAAGATCCAGGTTTCTGGGACTCTGAGGTCTGTGAGGCTTAC	783
Qy	221	GlyGlyAlaAsnGlyGlyProLeuAlaGlyValLysValLysAsnLeuLeuAsnGlyGlu	240
Db	784	GGCGCGCAGGGTGGAGGTCCATTGGCTGGTGTCAAGGTGAAGACTTGGTTACTGGGAAG	843
Qy	241	ValSerAspLeuGlnValSerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLys	260
Db	844	ATCTCCGACCTTCAGGTGTCCGGTCTCTTCTCGCCATCGACATGAACCGCGCAGAG	903
Qy	261	PheLeuGlyGlyGlnLeuGluLeuAspSerAspGlyTyrValGluThrLysProGlySer	280
Db	904	TTTCTCGCGCGCAGCTTGAGCTCGATGCTTGGTATGTGGCGACCAAGCCAGGCTCC	963
Qy	281	ThrHisThrSerValLysGlyValPheAlaAlaGlyAspValGlnAspLysLysTyrArg	300
Db	964	ACGCACACCAAGTGTGAAGGGGGTCTTGTCTCTGGGATGTGCGAGGACAGAGTATCGC	1023
Qy	301	GlnAlaIleThrAlaAlaGlySerGlyCysMetAlaAlaLeuAspAlaGluHisTyrLeu	320
Db	1024	CAGGCTATTACTGCGCTGGATCAGGGTGCATGCTCTTTGGACGCGGAGCACTATCTG	1083
Qy	321	GlnGluIleGlyAlaGlnGluGlyLysSerAsp	331
Db	1084	CAGGAGTCCGTGCACAGGAGGGCAAGCCGAT	1116
RESULT	3		
AKI06368		1383 bp	mRNA
LOCUS			linear
DEFINITION			Oryza sativa (japonica cultivar-group) cDNA clone: 002-102-C03, full insert sequence.
ACCESSION			AKI06368
VERSION			AKI06368.1
KEYWORDS			GI:32991577 FTI cDNA; oligo capping.

SOURCE ORGANISM	<i>Oryza sativa</i> (japonica cultivar-group) <i>Oryza sativa</i> (japonica cultivar-group) Eukaryota; Viridiplantae; Sireptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; <i>Oryza</i> .
REFERENCE AUTHORS	1 The Rice Full-length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-length cDNA Project Team, Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group: Otono,Y., Murakami,K., Iida,Y., Sugano,S., Fujimura,T., Suzuki,Y., Tsunoda,Y., Kurosaki,T., Kodama,T., Masuda,H., Kobayashi,M., Xie,Q., Lu,M., Nariikawa,R., Sugiyama,A., Mizuno,K., Yokomizo,S., Niikura,J., Ikeda,R., Ishibiki,J., Kawana,M., Yoshimura,K., Miura,J., Kusumegi,T., Oka,M., Ryu,R., Ueda,M., Matsubara,K., RIKEN: Kawai,J., Carninci,P., Adachi,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashidume,W., Hayatsu,N., Imotani,K., Arakawa,T., Fukuda,S., Kagawa,T., Kondo,S., Konno,H., Miyazaki,A., Osato,N., Ota,Y., Itoh,M., Saito,R., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Yoshino,M. and Hayashizaki,Y.
TITLE	Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice
JOURNAL MEDLINE PUBLISHED	Science 301 {5631}, 376-379 {2003} 22752273 12893764
REFERENCE AUTHORS	2 bases 1 to 1383) Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Doi,K., Fujimura,T., Fukuda,S., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayashizaki,Y., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hori,F., Hotta,I., Iida,J., Ikeda,R., Ikeda,R., Imamura,J., Imotani,K., Ishibiki,J., Ishii,Y., Ishikawa,M., Itoh,M., Kagawa,I., Kanagawa,S., Katoh,H., Kawagashira,N., Kawai,J., Kawamata,M., Kikuchi,S., Kishikawa-Hirozane,T., Kishimoto,N., Kobayashi,M., Kodama,T., Kojima,K., Kojima,K., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Kurosaki,T., Kusumegi,T., Li,C., Lu,M., Masuda,H., Matsubara,K., Matsuyama,T., Miura,J., Miyazaki,A., Mizuno,K., Murakami,K., Murata,M., Nagata,T., Nakamura,M., Namiki,T., Nariikawa,R., Niikura,J., Nishi,K., Nomura,K., Numasaki,R., Ohneda,E., Ohno,M., Ohtsuki,K., Oka,M., Ooka,H., Osato,N., Ota,Y., Otono,Y., Ryu,R., Saitoh,H., Sakai,C., Sakai,K., Sakagami,N., Sano,H., Sasaki,D., Sato,K., Satoh,K., Shibata,K., Shinagawa,A., Shiraki,T., Shishiki,T., Sogabe,Y., Sugano,S., Sugiyama,A., Suzuki,K., Suzuki,Y., Tegami,M., Tegami-Takeda,Y., Tagawa,A., Takahashi,F., Takaku-Akahiza,S., Tanaka,T., Tomaru,A., Toya,T., Tsunoda,Y., Ueda,M., Waki,K., Xie,Q., Yahagi,W., Yamada,H., Yamamoto,M., Yasunishi,A., Yazaki,J., Yokomizo,S. and Yoshimura,A.
TITLE	Direct Submission
JOURNAL	Submitted (27-AUG-2002) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan [E-mail:skikuchi@nias.affrc.go.jp, Tel:81-29-838-7007, Fax:81-29-838-7007]
COMMENT	This clone is one of the 28K full-length cDNA clones from japonica rice. URL : http://cdna01.dna.affrc.go.jp/cdna/NIAS Rice Full-length cDNA Project Team: Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and Yamamoto,M. FAIS Genome Sequencing & Analysis Group: Otono,Y., Iida,Y., Fujimura,T., Ikeda,R., Ishibiki,J., Kawamata,M., Kobayashi,M., Kodama,T., Kurosaki,T., Kusumegi,T., Lu,M., Masuda,H., Miura,J., Mizuno,K., Nariikawa,R., Niikura,J., Oka,M., Ryu,R., Sugano,S., Sugiyama,A., Suzuki,Y., Tsunoda,Y., Ueda,M., Xie,Q., Yokomizo,S., Yoshimura,A., Matsubara,K. and Murakami,K. Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hanagaki,T.,


```

QY 181 SerHisValTyrIleHisArgAenThrPheArgAlaSerIysIleMetGlnAla 200
D 648 TCCATGTGTACATCATCCACCGCCGCAACACCTTCGCGCCTCCCAAGATCATGCGAGCC 707
QY 201 ArgAlaLeuGluAsnProIysIleValLeuTyrPaspSerGluValValGluAlaTyr 220
D 708 AGGGGTTCACCAACCCCAAGATCCAGGTTCCTGAGCTCTGAGTCTCGAGGCCCTAC 767
QY 221 GlyGlyAlaAsnGlyGlyProLeuAlaGlyValIysValIysAsnLeuLeuAsnGlyGlu 240
D 768 GCGCGCGAGGGTGGAGTCCATTCGGTGGTCAAGGTCAAGAACTTGGTTACTTGGGAAG 827
QY 241 ValSerAspLeuGluValSerGlyLeuPhePheAlaIleGlyHisGluProAlaThrIys 260
D 828 ATCTCCGACCTTCAGTGTCCGCTCTCTTCCTTCGCCATCGGCATGAACCGCGACGAG 887
QY 261 PheLeuGlyGlyGlnLeuGluLeuAspSerAspGlyTyrValGluThrIysProGlySer 280
D 888 TTTCGCGCGGCGAGCTTCGAGTTCGATGCTGATGGTATGTGGCCACCAAGCCAGGCTCC 947
QY 281 ThrHisThrSerValIysGlyValPheAlaAlaGlyAspValGlnAspIysIysTyrArg 300
D 948 AGCGACACAGTGTGAAGGGGTCTTTCGCTGCTGGGATGTGCGACGACGAAGATATCGC 1007
QY 301 GlnAlaIleThrAlaAlaGlySerGlyCysMetAlaAlaLeuAspAlaGluHisTyrLeu 320
D 1008 CAGGCTATTCGCGCTGATCAGGTCATGGTCTGCTTGGACGCGGACATATCTG 1067
QY 321 GlnGluIleGlyAlaGlnGluGlyIysSerAsp 331
D 1068 CAGGAGGTGCGTGCACAGGAGGCGAAGCGCAT 1100

RESULT 2
LOCUS AK071251 1502 bp mRNA linear PLN 24-JUL-2003
DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone:J023087H21, full
insert sequence.
ACCESSION AK071251
VERSION AK071251.1 GI:32981274
KEYWORDS FLI CDNA; CAP trapper.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Euphorbioideae; Oryzeae; Oryza.

REFERENCE
1
AUTHORS The Rice Full-length cDNA Consortium, National Institute of
Agrobiological Sciences Rice Full-length cDNA Project Team;
Kikuchi,S., Satoh,K., Negata,T., Kawagashira,N., Doi,K.,
Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I.,
Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C.,
Ohtsuki,K., Shishiki,T., Foundation of Advancement of International
Science Genome Sequencing & Analysis Group; Ootomo,Y., Murakami,K.,
Iida,Y., Sugano,S., Fujimura,T., Suzuki,Y., Tsunoda,Y.,
Kurosaki,T., Kodama,T., Masuda,H., Kobayashi,M., Xie,Q., Lu,M.,
Narikawa,R., Sugiyama,A., Mizuno,K., Yokomizo,S., Niikura,J.,
Ikeda,R., Ishibiki,J., Kawamata,M., Yoshimura,A., Miura,J.,
Kusumegi,T., Oka,M., Ryu,R., Ueda,M., Matsubara,K., RIKEN;
Kawai,J., Carninci,P., Adachi,J., Aizawa,K., Arakawa,T., Fukuda,S.,
Hara,A., Hashidume,M., Hayatsu,N., Imotani,K., Arakawa,T., Itoh,M.,
Saito,R., Sasaki,D., Sato,K., Shibata,K., Shingawa,A., Osato,N., Ota,Y.,
Yoshino,M., and Hayashizaki,Y.
JAPONICA RICE
Collection, mapping, and annotation of over 28,000 cDNA clones from
japonica rice
Science 301 (5631), 376-379 (2003)
JOURNAL Science 301 (5631), 376-379 (2003)
MEDLINE 22752273
PUBMED 12669764
REFERENCE 2 (bases 1 to 1502)
AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Doi,K.,
Fujimura,T., Fukuda,S., Hanagaki,T., Hara,A., Hashizume,M.,
Hayashida,K., Hayashizaki,Y., Hayatsu,N., Hiramoto,K., Hiraoka,T.,
Hori,F., Hotta,I., Iida,J., Iida,Y., Ikeda,R., Imamura,K.,

```

```

Imotani,K., Ishibiki,J., Ishii,Y., Ishikawa,M., Itoh,M., Kagawa,I.,
Kagawa,S., Katoh,H., Kawagashira,N., Kawai,J., Kobayashi,M.,
Kikuchi,S., Kishikawa-Hirozane,T., Kishimoto,N., Kobayashi,M.,
Kodama,T., Kojima,K., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
Koya,S., Kurihara,C., Kurosaki,T., Kusumegi,T., Li,C., Lu,M.,
Masuda,H., Matsubara,K., Matsuyama,T., Miura,J., Miyazaki,A.,
Mizuno,K., Murakami,K., Murata,M., Nagata,T., Nakamura,M.,
Namiki,T., Narikawa,R., Niikura,J., Nishi,K., Nomura,K.,
Nunakami,R., Ohneda,E., Ohno,M., Ohtsuki,K., Oka,M., Ooka,H.,
Osato,N., Ota,Y., Ootomo,Y., Ryu,R., Saitoh,H., Sakai,C., Sakai,K.,
Sakazume,N., Sano,H., Sasaki,D., Sato,K., Satoh,K., Shibata,K.,
Shinagawa,A., Shiroki,T., Shishiki,T., Sogabe,Y., Sugano,S.,
Sugiyama,A., Suzuki,K., Suzuki,Y., Tagami,M., Tagami-Takeda,Y.,
Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A.,
Toya,T., Tsunoda,Y., Ueda,M., Waki,K., Xie,Q., Yahagi,W.,
Yamada,H., Yamamoto,M., Yasunishi,A., Yazaki,J., Yokomizo,S. and
Yoshimura,A.
Direct Submission
Submitted (08-DEC-2001) Shoshi Kikuchi, National Institute of
Agrobiological Sciences, Department of Molecular Genetics, Head of
Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki
305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp,
Tel:81-29-838-7007, Fax:81-29-838-7007)
This clone is one of the 28K full-length cDNA clones from japonica
rice.
URL : http://cdna01.dna.affrc.go.jp/cDNA/
NIAS Rice Full-length cDNA Project Team: Kikuchi,S., Satoh,K.,
Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,
Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and
Yamamoto,M.
FAJS Genome Sequencing & Analysis Group: Ootomo,Y., Iida,Y.,
Fujimura,T., Ikeda,R., Ishibiki,J., Kawamata,M., Kobayashi,M.,
Kodama,T., Kurosaki,T., Kusumegi,T., Lu,M., Masuda,H., Miura,J.,
Mizuno,K., Narikawa,R., Niikura,J., Oka,M., Ryu,R., Sugano,S.,
Sugiyama,A., Suzuki,Y., Tsunoda,Y., Ueda,M., Xie,Q., Yokomizo,S.,
Yoshimura,A., Matsubara,K. and Murakami,K.
Genome Exploration Research Group in Riken Genomic Sciences Center
and Genome Science Laboratory in Riken: Adachi,J., Aizawa,K.,
Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hanagaki,T.,
Hara,A., Hashizume,M., Hayashida,K., Hayatsu,N., Hiramoto,K.,
Hiraoka,T., Hori,F., Iida,J., Imamura,K., Imotani,K., Ishii,Y.,
Itoh,M., Kagawa,I., Kanagawa,S., Katoh,H., Kawai,J.,
Kishikawa-Hirozane,T., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
Nakamura,M., Nishi,K., Nomura,K., Nunakami,R., Ohno,M., Osato,N.,
Ota,Y., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H.,
Sasaki,D., Sato,K., Shibata,K., Shingawa,A., Shiraki,T.,
Sogabe,Y., Tagami,M., Tagami-Takeda,Y., Tagawa,A., Takahashi,F.,
Takahashi,A., and Hayashizaki,Y.
Location/Qualifiers
FEATURES
source
1..1502
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/db_xref="taxon:39947"
/clone="J023087H21"

Alignment Scores:
Pred. No.: 8,61e-125 Length: 1502
Score: 1590.00 Matches: 302
Percent Similarity: 96.37% Conservativeness: 17
Best Local Similarity: 91.24% Mismatches: 12
Query Match: 93.04% Indels: 0
DB: 8 Gaps: 0

US-10-005-429-25 (1-331) x AK071251 (1-1502)
QY 1 MetGluGlySerAlaAlaAAlaProLeuArgThrArgIleCysIleIleGlySerGlyPro 20
DB 124 ATGGAGGCGATCCGCGCGGCGCGCGCTCCGACGCGCGTGTGCATCATCGGAGCGGCGCG 183

```


AK104317 1389 bp mRNA linear PLN 24-JUL-2003
LOCUS Oryza sativa (japonica cultivar-group) cDNA clone.001-024-C03, full
DEFINITION insert sequence.
ACCESSION AK104317
VERSION AK104317.1 GI:32989526
KEYWORDS Oryza sativa (japonica cultivar-group)
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Eukaryota; Viridiplantae; Streptophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

1
REFERENCE
AUTHORS
The Rice Full-Length cDNA Consortium, National Institute of
Agronomical Sciences Rice Full-Length cDNA Project Team:
Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Xie, Q., Lu, M.,
Kishimoto, N., Yasaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I.,
Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C.,
Ohtsuki, K., Shishiki, T., Foundation of Advancement of International
Science Genome Sequencing & Analysis Group: Ohtsuki, K., Murakami, K.,
Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y.,
Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M.,
Narikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Niihara, J.,
Ikeda, E., Ishibiki, J., Kawamata, M., Yoshimura, A., Miura, J.,
Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN,
Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S.,
Hara, A., Hashidume, M., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M.,
Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Osato, N., Ota, Y.,
Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T.,
Yoshino, M. and Hayaishizaki, Y.

Collection, mapping, and annotation of over 28,000 cDNA clones from
japonica rice
JOURNAL Science 301 (5631), 376-379 (2003)
MEDLINE 22752273
PUBMED 12869764

2 (bases 1 to 1389)
REFERENCE
AUTHORS
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K.,
Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, M.,
Hayashizaki, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hiraoka, T.,
Hori, F., Hotta, I., Iida, J., Iida, Y., Ikeda, R., Imamura, K.,
Imotani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I.,
Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M.,
Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M.,
Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Kurosaki, T., Kusumegi, T., Li, C., Lu, M.,
Masuda, H., Matsubara, K., Matsuyama, T., Miura, J., Miyazaki, A.,
Mizuno, K., Murakami, K., Murata, M., Nagata, T., Nakamura, M.,
Namiki, T., Narikawa, S., Niihara, J., Nishi, K., Nomura, K.,
Numasaki, R., Ohneda, E., Ohno, M., Ohtsuki, K., Oka, M., Ooka, H.,
Osato, N., Ota, Y., Ohtsuki, K., Ohtsuki, K., Sakai, C., Sakai, K.,
Sakazume, N., Sano, H., Sasaki, D., Sato, K., Satoh, K., Shibata, K.,
Shinagawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S.,
Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami-Takeda, Y.,
Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A.,
Toya, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yahagi, W.,
Yamada, H., Yamamoto, M., Yasunishi, A., Yasaki, J., Yokomizo, S. and
Yoshimura, A.

Direct Submission
Submitted (27-AUG-2002) Shoshi Kikuchi, National Institute of
Agronomical Sciences, Department of Molecular Genetics, Head of
Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki
305-8602, Japan [E-mail:skkuchi@nias.affrc.go.jp,
Tel:81-29-838-7007, Fax:81-29-838-7007]
This clone is one of the 28k full-length cDNA clones from japonica
rice.
URL : <http://cdna01.dna.affrc.go.jp/cdna/>
NIAS Rice Full-Length cDNA Project Team: Kikuchi, S., Satoh, K.,
Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yasaki, J.,
Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T.,
Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T. and
Yamamoto, M.

PAIS Genome Sequencing & Analysis Group: Ohtsuki, K., Iida, Y.,
Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M.,

Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J.,
Mizuno, K., Narikawa, S., Niihara, J., Oka, M., Ryu, R., Sugano, S.,
Yoshimura, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S.,
Yoshimura, A., Matsubara, K., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Osato, N.,
Oka, Y., Satoh, K., Sakai, C., Sakai, K., Sakazume, N., Sano, H.,
Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tanaka, T., Tomaru, A.,
Toya, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yahagi, W.,
Yasunishi, A. and Hayaishizaki, Y.

Location/Qualifiers
1..1389
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="001-024-C03"

FEATURES
source
1..1389
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="001-024-C03"

ORIGIN
Alignment Scores:
Pred. No.: 9,22e-126 Length: 1389
Score: 1601.00 Matches: 303
Percent Similarity: 96.68% Conservative: 17
Best Local Similarity: 91.54% Mismatches: 11
Query Match: 93.68% Indels: 0
DB: 8 Gaps: 0

US-10-005-429-25 (1-331) x AK104317 (1-1389)
QY 1 MetGluGlySerAlaAlaAlaProLeuArgThrArgIleCysIleIleGlySerGlyPro 20
DB 108 ATGGAGGGATCCGGCGGGCGCGCGCTCCGACGCGCGTGTGCATCATCGGAGCGGCGC 167
QY 21 AlalaHieThrAlaAlaIleTyAlaAlaArgAlaGluLeuLysProValLeuPheGlu 40
DB 168 TCGCGCGCACACGCGGGGATCTACGCGCGCGCGCGGAGCTCAAGCCCGTCTCTTCGAG 227
QY 41 GlyTrpMetAlaAsnAspIleAlaAlaGlyGlyGlnLeuThrThrThrAspValGlu 60
DB 228 GCGTGGCTCGCCACAGACATCGCGCGGGGGGCGAGCTCACACACCGCGCGTGGAG 287
QY 61 AsnPheProGlyPheProAsnGlyIleMetGlyAlaAspLeuMetAspAsnCysArgAla 80
DB 288 AACCTCCCGGGTTCCCGCGAGGGGATCTCCGCGCGCGAGCTCATGGATCGCGCGGCC 347
QY 81 GlnSerLeuArgPheGlyThrAsnIleLeuSerGluThrValThrAlaValAspPheSer 100
DB 348 CAGTCCCTCCCGTTCGGCACCGCATATCTCCGAGACCGCTCACCGCGGTGCGATCTCTCC 407
QY 101 AlaCysPropPheArgValSerAlaAspSerThrThrValLeuAlaAspAlaValIleVal 120
DB 408 GCCTGCCCTTCGCGTCCCTCCGACTCCACACCGCTCGCGCGAGCGCGTGTGCTGTC 467
QY 121 AlatrGlyAlaValAlaAlaArgArgLeuHiePheProGlySerAspAlaTyTrpAsnArg 140
DB 468 GCCACCGCGCGCTCGCGCGCGAGTCCACTTCGCGCGCTCCGAGCGCTACTGGAACCGC 527
QY 141 GlyIleSerAlaCysAlaValCysAspGlyAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 160
DB 528 GGCATCTCCGCTCGCGCGTCTGGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 587
QY 161 AlaValIleGlyGlyGlyAspSerAlaMetGluLuserAsnPheLeuThrIleTyGly 180
DB 588 GCCCTCATCGCGCGCGGAGTCCGCCATGAGGAGTCCAACTTCTCTCCACCAATGACGCG 647

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model
Run on: May 5, 2004, 02:13:54 ; Search time 3993.73 Seconds
(without alignments)
3592.268 Million cell updates/sec

Title: US-10-005-429-25
Perfect score: 1709
Sequence: 1 MEGSAAPLRTRICIGSGP.....AALDAHYLQRIQAEQKSD 331

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlp
-O=/cpn2.1/USPTO.spool.p/US10005429/runat 04052004 121649 15437/app query.fasta_1.782
-DB=GenEmbl -QFMT=fastp -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blom62 -TRANS=human40.cai -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10005429 @CGN 1.1 5417 @runat 04052004 121649 15437 -NCPG=6 -ICPU=3
-NO XMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FCGAPOP=6
-FCGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
1: gb.ba.*
2: gb.htg.*
3: gb.in.*
4: gb.om.*
5: gb.ov.*
6: gb.pat.*
7: gb.ph.*
8: gb.pl.*
9: gb.pr.*
10: gb.ro.*
11: gb.sts.*
12: gb.sy.*
13: gb.un.*
14: gb.vi.*
15: em.ba.*
16: em.fun.*
17: em.hum.*
18: em.in.*
19: em.mu.*
20: em.om.*
21: em.ov.*
22: em.or.*
23: em.ph.*
24: em.pat.*
25: em.pl.*
26: em.ro.*
27: em.sts.*
28: em.un.*

29: em.vi.*
30: em.htg.hum.*
31: em.htg.inv.*
32: em.htg.other.*
33: em.htg.pln.*
34: em.htg.pln.*
35: em.htg.rod.*
36: em.htg.mam.*
37: em.htg.vrt.*
38: em.sy.*
39: em.htgo.hum.*
40: em.htgo.mus.*
41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match %	Query Length	DB ID	Description
1	1601	93.7	1389	8	AX104317 Oryza sat
2	1590	93.0	1502	8	AX071251 Oryza sat
3	1512	88.5	1383	8	AX106368 Oryza sat
4	1510	88.4	1045	8	TAB421947 Trifolium
5	1479	86.5	118300	8	AP004165 Oryza sat
6	1478	86.5	1560	6	AX366999 Sequence
7	1416	82.9	131980	2	AP005477 Oryza sat
8	1409	82.4	1130	6	AX654214 Sequence
9	1365	75.9	963	6	AX653785 Sequence
10	1335.5	78.1	1152	6	AX507791 Sequence
11	1335.5	78.1	1152	6	AX651358 Sequence
12	1315	76.9	1433	8	BT004322 Arabidops
13	1290	75.5	1021	6	AX366997 Sequence
14	1244.5	72.8	1261	8	ATTHIREDB
15	1227.5	71.8	76170	8	AC002329 Arabidops
16	1219	71.3	1148	8	ATTHIREDA
17	1218.5	71.3	27408	8	ATPISJ1
18	1218.5	71.3	197859	8	ATCHRIV83
19	1173	68.6	1128	8	AY099756 Arabidops
20	1023	59.9	31184	8	YSCD9476 Saccharomyc
21	1016	59.4	960	6	BD021847 Thiorodox
22	1011	59.2	963	6	AX488837 Sequence
23	1006	58.9	2592	8	SPU63113 Schizosacch
24	1006	58.9	3058	8	AF535134 Schizosacch
25	1006	58.9	17311	8	SPEC3F6
26	995	58.2	12130	1	AE011416
27	993.5	58.1	39954	8	YSCB8263
28	985	57.6	2134	8	SCU10274
29	972.5	56.9	1000	8	AF532986 Pneumocys
30	972.5	56.9	1129	8	AF532987 Pneumocys
31	933.5	54.6	17004	1	AE001616 Chlamydia
32	933.5	54.6	23099	1	AE002205 Chlamydia
33	933.5	54.6	300380	1	AE017158 Chlamydia
34	933.5	54.6	300650	1	AP002546 Chlamydia
35	929.5	54.4	110000	6	AR310754_03
36	922	53.9	2425	8	NEUCY59
37	913.5	53.5	12426	1	AE001284 Chlamydia
38	908.5	53.2	300512	1	AE016995 Chlamydia
39	907.5	53.1	11147	1	AE002304 Chlamydia
40	905	53.0	1423	6	AR008096 Sequence
41	900	52.7	339650	1	AP003583 Nostoc sp
42	898	52.5	1572	8	AF541944 Pneumocys
43	897	52.5	1423	8	PCRXB
44	894	52.3	298750	1	AP005375 X76119 Penicillium
45	877.5	51.3	5609	8	AY130996 Thermoosyn

ALIGNMENTS

RESULT 1

This Page Blank (uspto)

This Page Blank (uspto)

This Page Blank (uspto)

This Page Blank (uspto)